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SUMMARIES

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                                                                                                                                                                                   Score 19; DB Pred. No. 14;
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                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
                                                                                                                                                                                                                                                                             Homo sapiens clone 4 CC
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Vijh,S., Dayhoff,D.E., Wang,C.E.,
Direct Submission
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for a Rare TATA-less Promoter Structure
Drosophila and Humans
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                                 for a Rare TATA-less Promoter Drosophila and Humans
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                                                                   Transcription Regulation of Human Chemokine Receptor CCR3:
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                  80
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FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNL"
1 79 c 81 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="G-protein coupled receptor; principal eotaxin
receptor expressed on eosinophils, CD4 Th2 lymphocytes,
CD8 lymphocytes, microglia, dendritic cells, and
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/product="CC chemokine receptor
/protein_id="AAL85628.1"
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/mol_type="mRNA"
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/chromosome="3"
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1 (bases 1 to 410)

Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
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Vijh,S., Dayhoff,D.E.,
Direct Submission
                                                             Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Walter Reed Army Institute of Research, 1600 E. Gude Drive, Rockville, MD 20850, USA Location/Qualifiers
                                                                                                                             2 (bases 1 to 410)
Vijh,S., Dayhoff,D.E.,
Direct Submission
                                                                                                                                                                                                           Transcription Regulation of Human Chemokine Receptor CCR3: for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans Genomics 80 (1), 86-95 (2002)
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FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDQG"
a 93 c 98 g 108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="G-protein coupled receptor; principal eotaxin receptor expressed on eosinophils, CD4 Th2 lymphocytes, CD8 lymphocytes, microglia, dendritic cells, and
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/db_xref="taxon:9606"
/chromosome="3"
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                                              unidentified unidentified unclassified.
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19; Conserv
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Sequence 2 from Patent EP1012190.
AX030929
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Daugherty, B.L., Demartino, J.A., Siciliano,
Daugherty, B.L., Demartino, J.A., Sic
Eosinophil eotaxin receptor
Patent: EP 1012190-A 2 28-JUN-2000;
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FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISD"
91 c 96 g 110 t
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289 c 242 g
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/protein_id="AAL85631.1"
/db_xref="GI:19171647"
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from patent US 6271347.
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                        Demartino, J.A., Siciliano, S.J. and Springer, M.S.
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1 (bases 1 to 1065)

THORS Daugherty, B.L., Demartino, J.A., Springer

"LE Eosinophil eotaxin receptor

NAL Patent: JP 2002503950-A 1 05-FEB-2002;

MERCK & CO INC

OS Unidentified

PN JP 2002503950-A/1

PD 05-FEB-2000
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PN JP 2002503950-A/1
PD 05-FEB-2002
PF 24-APR-1997 JP 1997538970
PR 26-APR-1996 US 08/640991,26-APR-1996 US 17-JAN-1997 GB 9700894.0
Homo sapiens
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, SALVATORE J SICILIANO
PC C07K14/705, C07K14/715, C12N15/12
                                                                                                                                                                 Similarity
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Topology: Linear;
Eosinophil eotaxin receptor
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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19; Conserv
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE
KLERTSSVSPSTAEPELSIVF"
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/db_xref="GI:18093941"
/translation="MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLV
/translation="MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLV
FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFG
HGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVAAVFALRARTVTFGVITSIVTWGL
AVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVLFPLLVMAIL
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/mol_type="genomic DNA"
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mol_type="genomic DNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1068)

Xiao,L., Weiss,S., Qari,S., Rudolph,D., Hodge,T. and Lal,R.
Partial resistance to infection by syncytium-inducing primary HIV-1 in exposed uninfected individuals homozygous for CCR5 32bp deletion Unpublished

2 (bases 1 to 1068)
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Homo sapiens chemokine receptor
AF026535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1068)
Kato,H., Tsuchiya,N. and Tokunaga,K.
Direct Submission
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New variations of human CC-chemokine receptors CCR3 and CCR4 Genes Immun. 1 (2), 97-104 (1999)
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Homo sapiens gene for b-chemokine receptor CCR3, complete
AB023887
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/product="b-chemokine receptor CCR3"
/protein_id="BAA86964.1" ·
/protein_id="BAA86964.1" ·
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/translation="MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLV
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/mol_type="genomic DNA"
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/chromosome="3"
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Direct Submission
Submitted (24-SEP-1997) Retrovirus Diseases Branch, Centers
Disease Control and Prevention, 1600 Clifton Road, Atlanta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chemokine receptor 3
AY221092
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                                                                                                                                                                                        Submitted (20-JAN-2003) Guthrie cDNA Resource Center, Guthrie Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Kopatz,S.A., Aronstam,R.S. and Sharma,S.V. Isolation of complete coding sequence for cchemokine (C-C motif) receptor 3 (CCR3)
                                                                                                                                                                                                                                            2 (bases 1 to 1068)
Kopatz,S.A., Aronstam,R.S. and Sharma,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1068)
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/protein_id="AAB82589.1"
/db_xref="GI:2582566"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                   note="G-protein coupled receptor;
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Mammalian chemokine CCF18 and
BD015209
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Mammalian chemokine reagents

Patent: US 6512103-A 6 28-JAN-2003;

Location/Qualifiers
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AR278855
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JP 2001157593-A/4.
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Dairaghi, D.J., Hara, T., Miyajima, A.,
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                                                                                                                Mammalian chemokine CCF18 and receptor CCKR3 of mammal Patent: JP 2001157593-A 4 12-JUN-2001;
                                                                                                                                         Yoshimura, A.
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           04-OCT-2000 JP 2000305562
08-DEC-1995 US 08/567882
DANIEL J DAIRAGHI,TAKAHIKO HARA,ATSUSHI MIYAJIMA,THOMAS J
LL,WEI WANG,
AKIHIKO
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                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5
AR300123
AR300123.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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1 (bases 1 to 1116)
Mackay, C.R. and Ponath, P.D.
G-protein coupled receptor antagonists
Patent: JP 2001524068-A 3 27-NOV-2001;
LEUKOSITE INC
PN JP 2001524068-A/3
                                                                                                                  BD082062 111
G-protein coupled receptor
BD082062
BD082062.1 GI:22627672
BD 2001524068-A/3.
                                                                                                                                                                                                                                                                                                                                     Method of identifying inhibitors of C--C chemokine receptor Patent: US 6537764-A 5 25-MAR-2003; Location/Qualifiers
1. .1116
                                                                                                                                                                                                                                                                                                                                                                                        Unclassified.
1 (bases 1 to 1116)
Gerard, C.J., Gerard, N.P., Mackay, C.R.,
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                                                                                               Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N5/10,
C12N15/00,C12N5/00
Strandedness: Single;
Topology: Linear;
Topology: Linear;
Mammalian chemokine CCF18 and receptor CCKR3 of mammal
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 246
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
_292 c 242 g 30
                                                                                                                                                                                                                                                                                                              /organism="unknown"
286 c 257 g
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BD082061/c
LOCUS
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ORIGIN
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DEFINITION
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AR300122/c
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Sequence 3
AR300122
AR300122.1
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JP 2001524068-A/2.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1193)

Mackay, C.R. and Ponath, P.D.

G-protein coupled receptor antagonists
Patent: JP 2001524068-A 2 27-NOV-2001;
LEUKOSITE INC
                                                                                                                                                                                                 G-protein coupled receptor BD082061
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Gerard, C.J., Gerard, N.P., Mackay, C.R.,
                                                                                                                                                                                                                                                                                                                  CTGGGCCATCAGTGCTCTG 178
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24-SEP-1997 JP 1998516642
30-SEP-1996 US 08/720565
30-SEP-1996 US 08/720565
CHARLES R MACKAY, PAUL D PONATH
C07K16/18, C07K16/28, A61K39/395
Strandedness: Double;
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llarity 100.0%; Pred. No. 14
Conservative 0; Mismatches
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310 c 275 g
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
286 c 257 g 3(
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US 6537764.
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AR270522/c
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AX548778/c
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AR270522
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antigenic peptides
Patent: WO 02061087-A 63 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
                                                                 Burmer, G.C., Roush, C.L. and Brown, J.P.
Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second systems is a second system of the second systems for identifying such that the second system is a second system of the second systems for identifying such that the second system is a second system of the second systems for identification of the second systems is a second system of the second systems for identification of the second systems is a second system of the second systems is a second system of the second systems in the second system of the second system of the second systems is a second system of the second systems in the second system of the second systems is a second system of the second systems is a second system of the second systems in the second system of the second systems is a second system of the s
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AX548778
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Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1085 31-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown
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Mammalia; Eutheria;
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24-SEP-1997 JP 1998516642
30-SEP-1996 US 08/720565
CHARLES R MACKAY, PAUL D PONATH
C07K16/18,C07K16/28,A61K39/395
Strandedness: Double;
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1085 from patent US
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
310 c 275 g 3:
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Location/Qualifiers
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320 c 267 g
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                                                                                                                                                                                                                                                                                             GI:25813697
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Primates;
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Pred. No. 14;
0; Mismatches
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Pred. No. 14;
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6500938.
                                                                                                                                                                  Craniata; Vertebrata; Catarrhini; Hominidae;
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Submitted (07-JUN-1995) Christophe Combadiere, NIAID, National
Institutes of Health, Building 10, Room 11N111, Bethesda, MD 2
                                                                                                                                                                                                                                                                                                                                       On Feb 22, 1996 this sequence version replaced [Erratum J. Biol. Chem. 270 (1995) 30235].
Location/Qualifiers
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95348056
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1 (bases 1 to 1200)
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3 (bases 1 to 1201)
Combadiere, C., Ahuja, S.K. and Murphy, P.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning and functional expression chemokine receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemokine receptor J. Biol. Chem. 270
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                                                      /translation="MTTSLDTVETFGTTSYYDDVGLLCEKADTRALMAQFVPPLYSLV FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFG HGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGL AVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAIC YTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCERS KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE KLERTSSVSPSTAEPELSIVF"
320 c 267 g 336 t
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
320 c 267 g 33
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/product="CC chemokine receptor
/protein_id="AAC50469.1"
/db_xref="GI:1199580"
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  AR300121 1689 bp
Sequence 1 from patent US 6537764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-MAR-2000) Dept. of Mol. D. Walter Reed Army Institute of Research, Rockville, MD 20850, USA
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Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
Direct Submission
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1 (bases 1 to 1310)

Vijh,S.; Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
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llarity 100.0%;
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FTVGLLGNVVVVMILIKYRRLRIMT"
                                                                                                                                                                                                                                                                                                             CD8 lymphocytes, microglia,
                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                           /note="G-protein coupled receptor; principal eotaxin receptor expressed on eosinophils, CD4 Th2 lymphocytocles, microglia, dendritic cells, and
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PN JP 2001524068-A/1
PD 27-NOV-2001
PF 24-SEP-1997 JP 1998516642
PR 30-SEP-1996 US 08/720565
PI CHARLES. R MACKAY, PAUL D PONATH
PC C07X16/18, C07K16/28, A61K39/395
CC Strandedness: Double;
CC Strandedness: Double;
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Human C-C chemokine receptor 3
                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1689)

Mackay, C.R. and Ponath, P.D.

G-protein coupled receptor antagonists
Patent: JP 2001524068-A 1 27-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zea mays
Zea mays
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1 (bases 1 to 1689)
Gerard, C.J., Gerard,
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JP 2001524068-A/1.
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Location/Qualifiers
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416 c 344 g
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/db_xref="taxon:4577"
416 c 344 g 4
                                                                                                                                                                                                                                             organism="Zea mays"
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(CKR-3) gene, complete cds.
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U49727.1
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AX334894
AX334894.1 GI:18125613
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Molecular cloning and characterization of a human eotaxin receptor expressed selectively on eosinophils
J. Exp. Med. 183 (6), 2437-2448 (1996)
                 Patent: WO 0194629-A 5403 13-DEC-2001; Avalon Pharmaceuticals (US)
                                                      gene sets
                                                                     Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
                                                                                                                                                                                             Homo
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1 (bases 1 to 1689)
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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/product="C-C chemokine receptor 3"
/protein_id="AAB09756.1"
/db_xref="GI:147756.1"
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FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFG
HGMCKLLSGFYHTGLYSEIFFIILLTIDRYLAIVHAVFALRARTVTFGVITSIVTWGL
AVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAIC
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KLERTSSVSPSTAEPELSIVF"
416 c 345 g 497 t 1 others
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Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Daugherty, B.L.
Direct Submission
Submitted (13-MAR-1996) Bruce L. Daugherty, Inflammation Research,
Merck Research Labortories, R80W-107, P.O. Box 2000, Rahway, NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1717)

Daugherty, B.L., Siciliano, S.J., DeMartino, J.A., Malkowitz, L., Sirotina, A. and Springer, M.S.

Cloning, expression, and characterization of the human eosinophil
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J. Exp. Med. 183 (5), 2349-2354 (1996)
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U51241.1 GI:1480480
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428 c 351 g
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FTVGLLGNVVVVMILIKYRRLRIMTNIYLLNLAISDLLFLVTLPFWIHYVRGHNWVFG
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AVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAIC
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KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE
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428 c 351 g 50
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db_xref="GI:1480481"
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                                                                                                                                                                                                                                                                                                                                                 note="CC chemokine receptor-3; CCR3"
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ORGANISM
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BD017703/c
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BD006761/c
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PN JP 2001029089-A/2

PD 06-FEB-2001

PF 16-MAY-2000 JP 2000143832

PF 20-DEC-1995 US 08/575967,07-JUN-1996 US 08/661393 P

PATRICK W GARY, VICWKI L SHEICART, CARROLL J RAYPORT PC

PATRICK W GARY, VICWKI L SHEICART, CARROLL J RAYPORT PC

C12N15/09, C07K14/715, C07K16/24, C12N1/15, C12N1/19, C12N1/21, PC
                                                                                                                                                                                  BD017703 1915 bp DN#
Chemokine receptors 88-2B [CKR-3] and
BD017703
BD017703.1 GI:22558879
JP 2001264324-A/2.
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Gary, P.W., Schweickart, V.L. and Raport, C.J
Chemokine receptors 88-2B [CKR-3] and 88C,
Patent: JP 2001264324-A 2 26-SEP-2001;
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G01N33/53,G01N33/566//A61K39/395,A61K39/395,A61K45/00,A61P7/02, PC
A61P17/06,
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26-SEP-2001
28-DEC-2000 JP 2000401708
20-DEC-1995 US 08/575967,07-JUN-1996
                                          Unidentified 
JP 2001264324-A/2
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
470 c 373 g 58
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BC033514/c
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BC033514.1 GI:23958837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                      Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: n Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502636.
                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATRICK W GARY, VICKI L SCHWEICKART, CARROLL J RAPORT PC G01N33/50, A61K38/00, A61K45/00, A61P31/12, A61P31/18, C12Q1/02, C12Q1/70,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2030)
                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
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/= '88-2B polynucleotide and
Location/Qualifiers
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470 c 373 g 5
                                                      Location/Qualifiers
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AX705064
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5 from Patent WO03014153.
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AVLAALPEFIFYETEELFEETLCSALYPEDTVYSWRHFHTLRMTIFCLVLPLLVMAIC
YTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCERS
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Avlaalpefifyeteelfeetlcsalypedtvyswrhfhtlrmtifclvlpllvmaic
YTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCERS
XHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE
                                                                                                              KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE
KLERTSSVSPSTAEPELSIVF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="similar to chemokine (C-C motif) receptor /protein_id="AAH33514.1" /db_xref="GI:23958838" /db_xref="LocusID:1232" /db_xref="LocusID:1232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue_type="Brain, Lung, Testis, clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="MGC:34625 IMAGE:5176960"
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                                                                                                                                                                                                                                                                                     codon_start=1
                                                                                                                                                                                                                                                                                                      note="unnamed protein product"
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                                                                                              1285 c
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Pred. No. 14;
0; Mismatches
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AF247361/c
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MEDLINE
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Best Local Similarity
                 Query Match
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                                                                                                                  polyA_site
                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans Genomics 80 (1), 86-95 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, Military HIV Research Program, 1600 E. Gude Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 5791)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vijh,S., Dayhoff,D.E., Wang,C.E.,
Michael,N.L.
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AF247361
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/note="CCR3; G-protein coupled seven transmembrane
/note="CCR3; G-protein coupled seven transmembrane
spanning receptor; principle cell-surface receptor for
spanning receptor; principle cell-surface receptor for
spanning receptor; principle cell-surface on eosinophils,
cota/Th2 and CD8 lymphocytes, monocytes, microglia, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cione="lia5, frag B"
/cell_type="peripheral blood mononuclear cell"
<1. .5562
                                                                                                                       /gene="CCR3"
5562
                                                                                                                                                                             YTGIIKTLLRCPSKKKYKAIRLIFVIMAVFFIFWTPYNVAILLSSYQSILFGNDCERS
KHLDLVMLVTEVIAYSHCCMNPVIYAFVGERFRKYLRHFFHRHLLMHLGRYIPFLPSE
KLERTSSVSPSTAEPELSIVF"
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1285 c
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/gene="CCR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                                                                                                                         dendritic cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="CCR3"
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100.0%;
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Score 19;
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TITLE JOURNAL REFERENCE

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JOURNAL AUTHORS

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AC138069/c
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AC138069
AC138069.3
HTG.
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Submitted (13-JAN-2000) Basel Institute for Immunology,
Grenzacherstrasse, Basel CH-4005, Switzerland
Location/Qualifiers
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                                         Homo sapiens chromosome 3 clone RP13-546I2,
                                                    AC138069
                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CC chemokine 4318...4570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db xref="taxon:9606"
order(AF224496.1:298. .957,1. .>7010)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                          gene="CCR3"
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              GI:28416170
                                                                                                                                                                                                                                                                                                                                                                                                                _type=dispersed
                                                                                                                                                                                          100.0%; Score 19; DB 9; 100.0%; Pred. No. 15;
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Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-JAN-2003) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
4 (bases 1 to 177334)
Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z., Saenphimmachak,C., Buckley,D., Kibukawa,M., Raymond,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-DEC-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA 3 (bases 1 to 177334)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
Base-by-base quality values are not generally visible from GenBank flat file format but are available as part of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Overlapping Sequences:
5': RP11-793E15 (UWGC:bc0564) AC104439, 95469-bp overlap
                                                                                                                                                                                                                                             This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phre quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
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On Feb 19, 2003 this sequence version replaced gi:27573398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 177334)
Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haugen, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                         Sequence Validation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project Information
Center project name: chr-3
Center clone name: RP13-546I2 (bc0820)
Sequencing vector: plasmid; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: 177210 bases at least Q40
Consensus quality: 177313 bases at least Q30
Consensus quality: 177334 bases at least Q20
Insert size: 177334; sum-of-contigs
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: University of Washington Genome Center Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 9.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U95626, 42710-bp overlap
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digest

4857 6594 6656 8848 3818 4503 4468 1914 7718 5154 5136 1336 3818 4730 4713 11485 1 2376 13628 13324 974 868 1166 <800 2448 1674 9554 9494 373 5759 1398 1386 1003	5688 5759 3423 3409 1569 1539 5183 5363 73 <800 8078 8038 3100 3093 499 <800 1365 1325 921 959 723 <800 289 <800 4350 4244 2763 2834 11047 10790	2248 2269 6671 6656 3707 1074 1055 4052 4034 336 7303 7718 1392 1386 79 959 959 4253 4286 4736 1074 1055 2791 2834 1889 1074 1055 2647 2682 3696 1550 5750 2473 2400 1550	10027 4032 4034 875 886 5119 1846 1829 3716 375 1199 8334 8273 4502 452 1392 12882 12573 1967 194 2624 448 <800 2864 287 1674 12737 12573 4724 473 3818 10300 10103 4773 473	#ngrPrnt SequerMap FngrPrnt Fn	vector, in order to accurately represent the entire command of the fingerprint and hence do not a significant remaining discontinues the table. There are no significant remaining discontinues the experimental and predicted values. Unique fragments are separated by dashed lines. HindIII
SULT 38 104439/c CUS AC104439 FINITION Homo sapiens chromosom AC104439 AC024739 RSION AC104439.2 GI:2149024 YWORDS URCE Homo sapiens (human) Eukaryota; Metazoa; Ch Mammalia; Eutheria; Pr FERENCE 1 (bases 1 to 197279) AUTHORS Saenphimmachak, C., Phe	Query Match 100.0%; Score 19; DB 9; Length 177334; Best Local Similarity 100.0%; Pred. No. 15; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CTGGGCCATCAGTGCTCTG 19	6614 886 892 5694 <800 3255 1055 14484 3128 14484 1321 1321		7015 7139 219 <800 383 2852 2868 1571 1503 658 221 <800 154 <800 17 1002 1055 5077 5136 290 201 <800 2156 2190 250 6717 6864 1075 1089 38	1613 1641 178

Chemistry: Dye-terminator Big Dye; 6% of reads Assembly program: Phrap; version 0.99019 Consensus quality: 19725 bases at least Q30 Consensus quality: 19725 bases at least Q30 Consensus quality: 197275 bases at least Q30 Insert size: 197279; sum-of-contigs Ouality coverage: 8.2x in Q20 bases; sum-of-contigs Overlapping Sequences: 5': RPI1-9188 ([WGC:bc0216] AC026349 3': CTD-2563A18 ([WGC:bc0730)) Sequence Quality Assessment: This entry has been annotated with sequence quality estimates computed by the Bhrap assembly program. All manually estited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than leastly-base quality values are not generally visible from the General Clark file format but are available as part of this entry's ASN.1 file. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeate; all regions were covered by at least one plasmid subclone; and the assembly was confirmed by restriction digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cuteff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted remaining discrepancies between the experimental and predicted one appear in the cable. There are no significant remaining discrepancies between the experimental and predicted one appear	niver niver A., R D., R D., R D., R D., R One C one C
2509 3519 3519 26 26 26 27 28 28 29 29 29 29 20 20 20 20 20 20 20 20 20 20 20 20 20	2687 6382 512 449 2602 2590 2590 1711 9821 9821 9821 9821 7446
2617 3501 <800 933 <800 6410 115829 11877 4068 1683 <800 5082 115829 114296 1026 <800 6410 8291 1376 1471	2617 6410 <800 <800 2763 2617 8291 1683 9472 <800 8291 7581
631 402 402 1229 1229 1229 12332 674 674 11445 11445 1385 1385 1465 1385 1465 1747 1951	8949 2067 7846 7846 3734 1334 2287 1814 691 5477 305 25245 1633
<800 <800 3490 3490 4515 1183 4331 4121 2497 <800 2309 11045 5632 1414 <800 3895 11414 2497 <800 2309 2309	8586 2160 2160 7940 3895 1301 2309 1918 <800 5348 <800 25541 4121
4943 3239 1621 1621 1621 16418 16418 3361 3361 4220 4220 4220 4220 4615 6823 6823 6823 6823 7058 11547	8696 2742 2742 5376 1493 1493 1962 2900 1184 1181 1181 18560 3603
5076 3241 995 1615 6900 <8000 16263 3241 4193 22803 22803 2318 3241 4632 6900 881 2002 8661 1478 6900 1615	8661. <800 2803 5324 1478 835 2002 2954 1478 995 1171 1171 19002 3579

COMMENT

AUTHORS TITLE JOURNAL

RESULT 39 HSA312688/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE	Qy 1 Db 190292	Query Match Best Local S Matches 19													
HSA: HHSA: SEQUI AJ3: AJ3: HTG EUka EUka Mammu Mammu The Eur Eur 2199	1 CTGGGCCATCAGTGCTCTG	imi ';		2368	1711		7876 1911	1174	2854 6998	221	1002	6715		2738	3256
312688 22 Sapiens chromosome JENCING IN PROGRESS * 12688 2 GI:13559235; HTGS_PHASE2. D sapiens (human) D sapiens aryota; Metazoa; Chormalia; Eutheria; Prim malia; Eutheria; Prim s,H., Yang,Y., Kiss,Canski,J.P. transcriptional map transcriptional map 1921.3 J. Hum. Genet. 10 (196202) 10 Hum. Genet. 10 (196202) 10 Hum. Genet. 10 (196456) 10 (196205)	AGTGCTCTG	100.0%; larity 100.0%; Conservative 0		2389	1683	3847 5644	8291 1877	1145	2899 7317	<800	1026	6823	<800	2763	3278 3501
0965 bp 3 clone **, 26 data; C ates; C ates; C	19 190274	Score 19; Pred. No. 1 ; Mismatche	178 6589 3836	2811	388		249 2599	2152	237	3380	3255 5693	183	ω	10705	3700
- L - L - B		DB 9; Le 5; 8 0;	<800 6728 3895	2778	<800 2497	<800	<800 2778	2160	<800 <800	3317	3490 5632	<800	3317	10502	3666 1301
10 L 1. W		Length 197279; Indels 0;	4503 6607 2766	5159	13615		1613	1479	520 1540	219	154 1571	5077	2156	1078	2753 162
HTG 15-MAY-2002), *** Euteleostomi; Homo. imreh, S. and gion 1 (C3CER1)		Gaps 0;	4430 6900 2803	5076	13115 4632	9383	1615 1478	1478	<800 1478	<800	1478	5076	2173	1093	2803 8800
															

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202408-204878 bp Contig 23: 204979-213531 bp Contig 24: 213632-218109 bp Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.

* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced to be the submittor.

* This sequence will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kiss,H.

Direct Submission

Direct Submission

Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology

Submitted (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,

Center (MTC), Karolinska Institute, Tokaser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
Contig 4:
28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-6157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Apr 5, 2001 this sequence version replaced gi:13548633. The sequence is a consensus sequence of clone RP4-787c23 (1-140400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9: 117756-118727 bp Contig 10: 118828-121834 bp Contig 11: 121935-127855 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contigs are
in order and the gaps between them are represented by 100 Ns.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contig 20: 191476-201473 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127956-129383 bp Contig 13:
131848-132316 bp
Contig 15: 132417-134455 bp
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.89577-191375 bp
                                                                                                                                                                                                                                                                                                                                                                                                            11732
11832
26319
26319
28348
28448
42161
42361
55060
55160
61579
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97443
117756
1117756
                                                                                                                                                                                                                                                                                                                                                                                     118828
42360: gap of 55059: contig 61578: contig 61678: gap of 97342: gap of 117655: contig 117755: gap of 118727: contig 118827: gap of 121934: gap of 127955: gap of 127955: gap of 132948: gap of 132948: gap of 132316: gap of 132316: gap of 132316: gap of 133455: contig 133455: gap of 134455: contig 134555: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28347: contig
28447: gap of
42160: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on number will be preserved.

11731: contig of 11731 bp in length

11831: gap of 100 bp

26218: contig of 14387 bp in length

26318: gap of 100 bp

26318: gap of 100 bp

26317: contig of 2029 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig 13: 129484-131747 bp
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                                                                                                                                                                                                                                                                                                                                                                   of 100 bp
g of 20213 bp in length
of 100 bp
ig of 972 bp in length
of 100 bp
ig of 3007 bp in length
                                                                                                                                                                                                                                                 e 100 bp
g of 5921 bp i
e 100 bp
g of 1428 bp i
                                                                                                                                                                                         100 bp
of 2264 bp
     100 bp
of 972
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of 12699 bp in length
100 bp
of 6419 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
of 35664 bp in length
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of 13713 bp in length
                                                     100 bp
of 2039 bp in length
                                                                                                                    100 bp
of 469 bp in length
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     bp in length
                                                                                                                                                                                            in length
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                                                                                                                                                                                                                                                                                                                      in length
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REMARK
COMMENT
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BC030031/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORIGIN
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                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                             Direct Submission
Submitted (06-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                          Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC030031 1508 bp mRN Mus musculus, lymphocyte antigen 108, IMAGE:1225313, mRNA, complete cds. BC030031
                                                                                                 cDNA Library Preparation: Soares Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org
                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; (bases 1 to 1508)
                                                                                                                                                                                                                                                                                                                                                                                                                          BC030031.1 GI:20988098 MGC.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                  contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                        Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCATCAGTGCTCTG 140350
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202308
202408
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218110
218210
219801
                                                                                                                                                                                                                                                                                                                                                                                                         musculus (house mouse)
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DN
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/chromosome="3"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202307: contig of 734 bp in length
202407: gap of 100 bp
204878: contig of 2471 bp in length
204978: gap of 100 bp
213531: contig of 8553 bp in length
213631: gap of 100 bp
218109: contig of 4478 bp in length
218209: gap of 100 bp
219800: contig of 1591 bp in length
219900: gap of 100 bp
220965: contig of 1065 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lone="RP6-32g23"
44674 c 45661 g
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75: contig of 1799 bp in length
5: gap of 100 bp
3: contig of 9000
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contig of 325 bp
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Pred. No. 15;
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of 53424 bp in length
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2600 others
                                                Mark Ketteman, Anuradha and Michelle Whiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 220965;
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B MGC:41003
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SOURCE

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BASE COUNT
ORIGIN
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Search completed: January 13, 2004, 17:57:07 Job time : 747 secs
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Matches 18
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This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 1
Location/Qualifiers
                                                                                                                                                                              Similarity
                                                                                CTGGGCCATCTGTGCTCTG
                                                                                                         CTGGGCCATCAGTGCTCTG
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                           /db_xref="LocusID:30925"
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TCQIHLACVLKNQSQTVSVEWQATGNISLGGPNVTIFWDPRNSGDQTYVCRAKNAVSN
ISVSVSTQSLCKGVLTNPPWNAVWFMTTISIISAVILIFVCWSIHVWKRRGSLPLTSQ
HPESSQSTDGPGSPGNTVYAQVTRPMQEMKIPKPIKNDSMTIYSIVNHSREETVALTG
                                                                                                                                                                                                                                                            YNQPITLKVNTLINYNS"
342 c 321 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="MGC:41003 IMAGE:1225313"
/tissue_type="Thymus gland, mous
/clone_lib="Soares_thymus_2NbMT"
/lab_host="DH10B"
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/protein_id="AAH30031.1"
/db_xref="GI:20988099"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL/6J"
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94.7%;
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Maximum Match 100%
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic - nucleic search, using sw model
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          January 13, 2004, 15:53:18; Search time 1192.5 Seconds (without alignments) 387.241 Million cell updates/sec
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gb_htc: *
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60693 D027513 R	AF160693	9	9	9	43
95355 RPCI-23-	8 AQ99	85	σ,	ο,	42
M141543 ZFT407 Z	2 BM14:	85		ა	41
57791 fl10g10	0 BESS	72	9		40
Q074707 fz24f09.	BQ07	27		ა	39
96684 fb48	AI496	02		16.4	38
500347 WHE4018	4 CA50	96	ი	ა	37
670955 fp:	2 BI67	91		٥.	36
074936 fz24f09.	3 BQ07	74	ი	ა	35
616929 fab02a02	3 BQ61	36		٥.	34
BG891847 fp45e01.x	2 BG89:	28	9	٥,	33
728994 fp06g01.	0 BG721	22	<u>.</u>	9	32
473885 fp48b06.	2 BI47:	77	٠ ص	9	31
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786165 2M0031F0	8 AZ78	31		რ.	28
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AW594895 £k26a06.y	AW594895	27	٥.	16.4	24
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0567 Triticum	AL81056	137		6	20
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27989 602	0 BG3279	79	_	7.	18
58742 Tet	9 CNS038	070	Ľ	7.	17
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21494 602	2 BG8214	00	_	7	15
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36792 603	2 BI8367	20	_	17.4	13
821578 602	2 BG8215	69	1	17.4	12
824723 602	2 BG8247	38	_	7.	11
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G182330 RST119	0 BG1823	84	8		_ر

ALIGNMENTS

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LOCUS
DEFINITION
RST73417 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION
BG204024
SET.
BG204024.1 GI:13725711
REYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
CORGANISM
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 745)
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SUMMARIES

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BG204024 BG205056 BI821796 BI906283

BG204024 RST23417 BG205056 RST24475 BI821796 603035872 BI906283 603063222

Description

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REFERENCE
AUTHORS
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1 (bases 1 to 789)

1 (bases 1 to 789)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Harrington, J., Sherf, B., Thornton, M., Ramachandran, R., Whittington, J., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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High quality sequence stop
                                                                                                                                                                                                                                                                                                                                                                                         3201 Carnegie Ave, Cleveland, Tel: 216 431 9900 Fax: 216 361 9596 Email: gcain@athersys.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BG205056.1 GI:13726743
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RST24475 Athersys RAGE Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Scott J. Cain Atherays, Inc.
                                                                                                                                                                                                                                                                                                                                                                  High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                       scain@athersys.com
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/clone lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 207 c 170 g 209 t
                                                /clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 207 c 183 g 222 t 3 others
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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 DB 10;
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
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B1906283/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11440 row: p column: 17
High quality sequence start: 2
High quality sequence stop: 750.
Location/Qualifiers
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                                                      BI906283 876 bp mkNA LIHER 603063222F1 NIH_MGC_118 Homo sapiens cDNA clone
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
mRNA sequence.
BI906283
BI906283.1 GI:16168946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                               /clone libe"NIH_MGC 115"
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5176960"
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                                                                                                                                                                                                                                                                               Score 19; DB 12;
Pred. No. 2.1e+02;
; Mismatches 0;
                                                                                     876 bp
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                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 884)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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RST1196 Athersys RAGE Library
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Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Homo sapiens
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Contact: Scott J. Cain
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
/note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: PCMV-SPORT6; Site_
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/tissue_type="leukocyte"
/lab_host="DH10B"
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mol_type="mRNA"

/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 934)

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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RST43688 Athersys RAGE Library
BG460984
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High quality sequence stop
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3201 Carnegie Ave,
                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Scott J. Cain
Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG460984.1
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Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
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216 361 9596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
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/db_xref="taxon:9606"

/cell line="HT1080"

/clone lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

Nature Biotechnology, in press. Note that even though the

cell type indicated is HT1080, since a random activation

method was used, these sequence tags are not necessarily

expressed in HT1080 under normal circumstances."

91 a 231 c 206 g 256 t
                                                                                                                                                                                                                                                                                                                      scain@athersys.com.
/clone_lib="Athersys RAGE Library"
/clone_"See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 188 c 237 g 282 t 27 others
                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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Sutheria; Primates; Catarrhini; Hominidae; Homo.
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2.1e+02;
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VERSION KEYWORDS SOURCE

ACCESSION

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RESULT 7
AQ571744
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                                                                                                                                                                                                BASE COUNT
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Best Local
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                                                                                                           Best Local
                                                                                                                             Query Match
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 174
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                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 451)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ571744 451 bp DNA linear GSS 01-JUN-1999
HS_5380_B2_H12_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=956 Col=24 Row=P, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: 956 row: P column: 24
Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.htsc.washington.edu
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                                            CTGGGCCATCAGTGCTCTG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 451
Location/Qualifiers
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                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC ends
                                                                                                                                                                                     /Clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
/note="Vector bBACe3.6; Site 2: EcoRI and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

132 c 110 g 108 t
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                         clone="Plate=956 Col=24 Row=P"
                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
                                                                                                       91.6%;
94.7%;
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 192
                                                                                                         Score 17.4;
Pred. No. 8.
                                                                                    Mismatches
                                                                                                       8.6e+02;
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BY758727/c
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                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda
,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K.,
Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno
,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y.,
Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construence dundant cDNA library. Genome Res. 11 (2), 281-289
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22354683
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BY758727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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Jutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                          construction of a
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                                                                                           Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 703)

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 bp mRNA linear EST 1. BB089480 RIKEN full-length enriched, 12 days embryo, embry between diaphragm region and neck Mus musculus cDNA clone 9430022H21 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
On Jun 21, 2000 this sequence version replaced gi:8655274.
Contact: Yoshihide Hayashizaki
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                  Tel: 81-45-503-9222
Fax: 81-45-503-9216
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                  Hayashizaki,Y.
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/cell_line="CRL-1722 L5178Y-R"
/clone_lib="RIKEN full-length enriched, CF
149 c 152 g 174 t 3 others
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/strain="DBA/2"
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Pred. No. le
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                                                                                                                                                                                                                                                                                                          BGB21437 737 bp mRNA linear BST 22-MAY-2001 602724894F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4864654 5',
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 737)

NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                  mRNA sequence.
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Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                           BG821437.1 GI:14169024
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                                                National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                         sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        embryonic body between diaphragm region and neck"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
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/lab_host="DH10B"
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94.7%;
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Pred. No. 1.
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Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LicM1728 row: k column: 23
High quality sequence stop: 734.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 738)
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                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                           Plate: LLCM1737 row: j column: 01
High quality sequence stop: 728.
Location/Qualifiers
                                                                                                                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/clone_lib="NIH_MGC_15"
/clone_lib="NIH_MGC_15"
/clone_lib="NIH_MGC_15"
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/corI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
70 a 214 c 223 g 130 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4864654"
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                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4868064"
/tissue_type="adenocarcinoma cell line"
                                                                                                   organism="Homo sapiens"
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Pred. No. 1.1e+03;
0; Mismatches 1;
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BASE COUNT
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BG821578/c
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Query Match
Best Local Similarity
Matches 18; Conserv
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BG821578
BG821578.1 GI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution informatic found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLCM1728 row: p column: 17 High quality sequence stop: 692.
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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/clone_lib="NIH_MGC_15"
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ECORI; cDNA made by oligo-dT priming. DTrectionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
68 a 211 c 229 g 130 t
     Conservative
                                                                                                   /tissue_type="adenocarcinoma cell line"
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/clone_lib="NH1 MGC_15"
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82 a 217 c 235 g 135 t
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'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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94.7%;
                         91.6%;
94.7%;
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Pred. No. 1.1e+03;
      Score 17.4; DB 12;
Pred. No. 1.1e+03;
0; Mismatches 1;
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CTGGGCCATCAGTGCTCTG

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BI836792
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Best Local (
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11563 row: k column: 18
                                                                                                                       898 BG822063 898 602726178F1 NIH_MGC_15 Homo mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 635.
Location/Qualifiers
                  Homo sapiens (human)
                                                                                BG822063.1 GI:14169650
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="NIH_MGC 120"
/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

90 a 219 c 245 g 151 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5224073"
/lab_host="DH10B"
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94.7%;
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Pred. No. 1.1e+03;
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JOURNAL COMMENT
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cDNA Library Preparation: Ling Hong/Rubin Laboratory, cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: NIH Intramural Sequencing Center Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1728 row: h column: 18 High quality sequence stop: 808. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (I
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution informatic
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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1 (bases 1 to 900)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
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BG821494.1 GI:14169081
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National Institutes of Health, Mammalian
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/clone="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. DTrectionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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AL234743.1 GI:7893878
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                         Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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/tissue_type="adenocarcinoma cell line"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_15"
/clone_lib="NIH_MGC_15"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
/no
Location/Qualifiers
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mol_type="mRNA"
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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054A19 of
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                    /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="054A19"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG0
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/db_xref="taxon:99883"
/clone="008L02"
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                                                      AK034665 1817 bp mRNA linear HTC 05-DEC-2002 Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430022H21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CTGGGCCATCAGTGCTCTG 19
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1 (bases 1 to 1579)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602427610F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE: 4546899
               product:unknown EST, AK034665
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High quality sequence stop: 197.
Location/Qualifiers
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH_MGC 15"
/clone lib="NIH_MGC 15"
/note="Organ: colon; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
75 a 773 c 218 g 113 t
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/mol_type="mRNA"
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

All Nature 420, 563-573 (2002)

6 (bases 1 to 1817)

Radachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Havashiraki Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria;
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RESULT 20
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SV AL810567:
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                                                                                Wilson I., Beswick R., Shepherd S., Barker Edwards D., Coghill J., Holdsworth M., Lent "A BBSRC-funded wheat EST resource for the
                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea Triticeae; Triticum.
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02-SEP-2002
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                                                                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
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Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rigenomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel.
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match=477)"
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'clone_lib="RIKEN full-length
'dev_stage="12 days embryo"
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Hayashizaki,Y.
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                                                                                Barker G., Parker J., Ow M., Lenton J., Shewry P., for the academic communit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 137
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                                                                                                                                                                                                                  This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC1&t2=RC1-NN0233-221100-011-a03&t3=2000-11-22&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF
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Mammalia; Eutheria;
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                                                                                                                                                         High quality sequence stop: 178.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
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/clone_lib="e:29"
/clone="D11_e29_plate_4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 A; 26 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Triticum aestivum"
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'mol_type="mRNA"
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94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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CA912316/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bui, A.Q., Le, B.H., Weterings, K., Bi, Y.-P., Choi, J.-S., McElroy, K, Choi, P.S., Harada, J.J., Fischer, R.L. and Goldberg, R.B. Gene Activity in Different Regions of a Post-Fertilization Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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17; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Molecular, Cell, & Developmental Biology University of California, Los Angeles 621 Charles E. Young Drive South, Los Angeles, CA 9009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
Phaseolus coccineus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: bobg@ucla.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 310 825 3270 Fax: 310 825 8201
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/dev_stage="6-days post-pollination"
/clone lib="Scarlet Runner Bean Suspensor Region TriplEx2"
/note="Organ: Suspensor Region of Globular-Stage Embryos;
/note="Organ: Suspensor Region of Globular-Stage Embryos;
/ector: TriplEx2; Site_1: SfiIA; Site_2: SfiIB; Suspensor regions were micro-dissected from globular-stage embryos six days after pollination from greenhouse-grown plants [Weterings et al., Plant Cell 13, 2409-2425 (2001)].

Double-stranded cDNA was synthesized from suspensor mRNA using the SMART cDNA Library Construction Kit according to the manufacturer (Clontech). The suspensor cDNA fragments were directionally ligated into the SfiI restriction site of the lambda TriplEx2 vector (Clontech), and the recombinant cDNAs were transformed into E. coli XL1-Blue cells (Clontech). Suspensor cDNA plasmids used for directional sequencing were obtained by in vivo excision from the lambda TriplEx2 recombinants in E. coli BM25.8
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/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
/note="Organ: nervous normal; Vector: products
derived from ORESTES PCR (U.S. Letters Patent application
NO. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
37 c 40 g 56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cultivar="Hammond's Dwarf Scarlet"
db_xref="taxon:3886"
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∏OI
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Pred. No. 1.
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1 (bases 1 to 322)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
17; Conserv
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-BN0238-010800-001-e03&t3=2000-08-01&t4=1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
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Location/Qualifiers
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/note="Organ: breast normal; Vector: pucl8; Site_1: SmaI;
/note="Organ: breast normal; Vector: pucl8; Site_1: SmaI; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                              issue mRNA and cDNA amplification were performed under ow stringency conditions."

64 c 59 g 86 t
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Score 16.4; DB 10
Pred. No. 2.1e+03;
0; Mismatches 1
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les 17; Conserv
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1 (bases 1 to 327)
1 (bases 1 to 327)
Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy
Clark, M., Johnson, S.L., Martin, J., Beck, C., Wylie, T., Underwood
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
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Fax: 314 286 1810
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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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EST.
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   CC469335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU Zebrafish EST Project 1998
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/tissue_type="1 day fin regenerates"
/lab_host="E. coli XLOLR"
/clone_lib="zebrafish fin day1 regeneration"
/clone_lib="zebrafish fin day1 regeneration"
/note="vector: pBK-CMV; Site_1: ECORI; Site_2: XhoI; 1st
strand cDNA primed with (GA) IOACTAGTCTCGAG(T)18, followed
by second strand synthesis, and ligated to 5' adapter (5')
-aattcggcacgag-3', 3'-gccgtgctc-5'. cDNA was cloned
directionally (EcoRI/XhoI) into Stratagene Zap express
lambda phage arms. Mass invivo excision done to obtain
inserts in pBK-CMV phagemid."
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REFERENCE
AUTHORS
TITLE
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KEYWORDS
SOURCE
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CB806515/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Cientifico e Tecnologico (CNPq), Brazil.

Plate: 141 row: P column: 20

Seq primer: T7
                                                                                                          CB806515 386 bp mRNA AMGNNUC:NRDG1-00115-A10-A nrdg1 (10855) clone nrdg1-00115-a10 5', mRNA sequence. CB806515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embrapa Recursos Geneticos e Biotecnologia
Parque Estacao Biologica, Final Av. W/5 No.
02372, 70770-900 Brasil
Tel: 55 61 448 4778
Fax: 55 61 340 3658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 381)
Costa, J.N., Mota, M. and Caetano, A.R.
Brazil's Contribution to End-Sequencing the Bovine BAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence CC469335
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Contact: Caetano AR
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                                        CB806515.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 381.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Rattus norvegicus (Norway rat)
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/clone lib="CHORI-240"
/clone lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; S
/note="Vector: pTARBAC1.3; Site_1: MboI; Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_141P20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /вех="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Bos taurus"
                                                                              GI:29924649
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Pred. No. 2.3e+03;
0; Mismatches 1;
                                                                                                                                                                                                      Rattus norvegicus
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BY596515/c
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Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pestovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wang, L.G., Wynshaw-Boris, A., Yanagisawa, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander
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Mus musculus (house mouse)
Mus musculus
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BY596515 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930050L08 3', mRNA sequence.
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Tel: 805 447-4881
Plate: 00115 row
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Amgen EST Program.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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61 c 82 g
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/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="nrdg1-00115-a10"
/tissue type="Dorsal Root Ganglia"
/clone_Tib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1;
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Pred. No. 2.3e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                      173
                                                                                                     AZ786165
431 bp DNA linear GSS 102M0031F02R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC2M0031F02 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity 17; Conserv
                        AZ786165.1
GSS.
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The Institute of Physical and Chemical Research (RIKEN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Miyazaki,A.,
,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A.,
,Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K.,
,Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami
,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
90 c 118 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
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                                                      GI:12923652
                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                             Score 16.4; DB 13;
Pred. No. 2.4e+03;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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musculus (house mouse)

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                                                                                                                                                                                                                                   384
                                                                                                                                                                                                                                                                                                                           17;
AQ706454
HS_5554_A1_G06_SP6E_RPCI-11 Human Male genomic_clone Plate=1130 Col=11 Row=M, AQ706454
AQ706454
AQ706454.1 GI:5415880
GSS.
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: F column: 02
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
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                                                                                                                                                                                                                                                                             CTGGGCCATCAGTGCTCT
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=\overline{\ }^{-1}Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'mol_type="genomic DNA"
'strain="C57BL/6J"
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94.4%;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 28;
Pred. No. 2.4e+03;
0; Mismatches 1;
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                                                                   linear GSS
BAC Library Homo
genomic survey se
                                                                                                                                                                                                                                                                                                                                                                    Length 431;
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AZ813275
LOCUS
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1 (bases 1 to 460)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
                         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 474)
1 (bases 1 to 474)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Pedersen,T., Reilly Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ813275

2M0080A05R Mouse 10kb plasmid UUGC1M library Mus clone UUGC2M0080A05 R, genomic survey sequence.
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Plate: 1130 row: M column: 11
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                    GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 460.
Location/Qualifiers
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
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Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ813275.1 GI:12983183
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whole genome scaffolding with paired end reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and partially digested with a combination of EcoRI EcoRI Methylase. Size selected DNA was cloned into pBACe3.6 vector at EcoRI sites"
71 c 123 g 97 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="RPCI-11 Human Male BAC Library" /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen displayed by the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=1130 Col=11 Row=M"
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94.4%;
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Rodentia;
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RESULT 31
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                                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: A column: 05
Seq primer: CACACAGGAAACAGCTATGACC
; CYPITHICA, ------; Chases 1 to 477)

1 (bases 1 to 477)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Clark,M., Johnson,S.L., Martin,J., Beck,C., Wylie,T., Un, S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Un
                                                                                                                                                                                                                                                                                            BI473885
477 bp mkNA linear bor fp48b06.y3 zebrafish gridded kidney Danio rerio cDNA clone IMAGE:4759643 5' similar to SW:IAP CHICK Q90660 INHIBITOR OF APOPTOSIS PROTEIN ;, mRNA sequence.
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Location/Qualifiers
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid inserts
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                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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BI473885.1 GI:15302437
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone_lib="Mouse 10kb plasmid UUGC1M library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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94.4%;
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TITLE
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AUTHORS
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BG728994
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                                                                                          i (bases 1 to 522)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwoo,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Ko, Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                 BG728994 522 bp mRNA linear EST 09-fp06g01.x1 zebrafish gridded kidney Danio rerio cDNA clone IMAGE:4728769 3' similar to SW:IAP_CHICK Q90660 INHIBITOR (APOPTOSIS PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.genomesystems.com) (email contact: info@genomesystems.com) and
Research Genetics, Huntsville, Alabama (web address: www.resgen.com)
) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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WashU Zebrafish EST Project 1998
Unpublished
Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                 Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                           BG728994.1 GI:14014069
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Possible reversed clone: similarity
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/note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; Oligo dT cDNA library constructed from r
pooled from pooled kidney tissue from 300 adult
zebrafish."
109 c 96 g 158 t
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mol_type="mRNA"
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clone="IMAGE:4759643"
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94.4%;
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Pred. No. 2.5e+03;
0; Mismatches 1
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RESULT 33
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AUTHORS
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy , S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood , K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:
Washington University Genome Sequencing Center Clone distribution:
Genome Systems, St. Louis, Missouri (web address:
                                                                                                 Unpublished
Contact: Stephen L. Johnson
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
Tel: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG891847 528 bp mRNA linear EST 04-JI fp45e01.x1 zebrafish gridded kidney Danio rerio cDNA clone IMAGE:4759752 3' similar to SW:IAP_CHICK Q90660 INHIBITOR OF APOPTOSIS PROTEIN ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                      WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                 and Wilson, R.
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Location/Qualifiers
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/note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; Oligo dT cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
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/db_xref="taxon:7955"
/clone="IMAGE:4728769"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="kidney pooled from 300 wild type adults" lab_host="XLOLR"
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Pred. No. 2.
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Teleostei;
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Ostariophysi; Cypriniformes
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BQ616929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ616929 536 bp mRNA linear EST 26-
fab02a02.x1 Sugano SJD adult male Danio rerio cDNA clone
IMAGE:6034059 3' similar to SW:IAP2_HUMAN Q13490 INHIBITOR
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Danio rerio
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Research Genetics, Huntsville, Alabama (web address: www.resgen.com)
) (email contact: info@resgen.com) and
                                                                                                                               Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakan Sequencing by: Washington University Genome Sequencing Center distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                            Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
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                                                                                                                                                                                                                                                                                                                                                             Unpublished
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/note="Organ: kidney; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; Oligo dT cDNA library constructed from
pooled from pooled kidney tissue from 300 adult
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/db_xref="taxon:7955"
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
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                                                                                        Location/Qualifiers
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Pred. No. 2.7e+03;
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Ostariophysi; Cypriniformes
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RESULT 35
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                                                                                                                                                                                                             The library was constructed by Dr. Z. Gong. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Please contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260). Seq primer: T3 ET from Amersham High quality sequence stop: 424.
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Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., ,K., Steptoe,M., Theising,B., Allen,M., Schurk,R., Ritter,E., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Danio rerio
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BQ074936
BQ074936.1 GI:19903973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/dev_stage="adult"
/lab_host="DH10B (phage resistant)"
/clone_lib="Sugano SJD adult male"
/note="Vector: pME18S-FL3; Site_1: DraIII (CACCATGTG);
Site_2: DraIII (CACTGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT];
double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed and donated by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CGACCTGCAGCTCGAGCACA. "
32 a 126 c 107 g 171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zebrafish EST Project 1998
                                                                                                                 organism="Danio rerio"
/mol_type="mRNA"
                                                                                            xref="taxon:7955"
_stage="4-5 month"
_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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ACCESSION VERSION

DEFINITION

KEYWORDS

SOURCE ORGANISM

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BASE COUNT ORIGIN

REFERENCE AUTHORS

COMMENT

FEATURES

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JOURNAL COMMENT
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VERSION
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DEFINITION
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BI670955
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ORIGIN
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                        Email: zbrafish@watson.wustl.edu
Library constructed by: Chandra Tucker and Gregory Niemi DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: RessourcenZentrumPrimarDatenbank, Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                i (bases 1 to 591)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy (S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, B., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Chark, M., Caron B., Waterston B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI670955

S91 bp mRNA linear EST 13-FEB-2002 fp58f06.x1 Zebrafish adult retina cDNA Danio rerio cDNA clone IMAGE:4786307 3' similar to SW:IAP_CHICK Q90660 INHIBITOR OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                           (web address: www.rzpd.de)
Seq primer: T7 from Gibco
High quality sequence stop: 389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished Other_ESTs: fp58f06.y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI670955.1 GI:15586339
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314 286 1810
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                                                                                                                           /organism="Danio rerio"
/mol_type="mRNA"
/strain="wild-type"
/db_xref="taxon:7955"
/clone="IMAGE:4786307"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
106 c 154 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Gong zebrafish testis"
/note="Organ: testis (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the testes of 31 male adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
/dev_stage="1-2 years"
/lab_host="E.Coli XL1-Blue MRF' (XL1-Blue MRF')"
/clone_lib="Zebrafish adult retina cDNA"
/note="Vector: Lambda ZAP II (pBluescript SK-); Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University protocol
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                                                                                                          'sex="mixed"
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94.4%;
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Pred. No. 2.8e+03;
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CA500347/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Unpublished
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
West Area, Western Regional Research Cushanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WHE4018_D05_G10ZT Wheat meiotic anther cDNA linear EST 14-NOV-2002 aestivum cDNA clone WHE4018_D05_G10, mRNA sequence. CA500347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: oandersn@pw.usda.gov
Sequences have been trimmed to rem
quality sequence with phred score
Seq primer: T7 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 596)
Anderson,O.D., Chao,S., Crossman,C., Langridge,P., Lazo,G.R., Pham,J., Rausch,C.J., Sutton,T., Woo,J. and Wilson,C.
The structure and function of the expressed portion of the wheat genomes - Meiotic anther cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Triticeae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA500347.1 GI:24991307
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (bread wheat)
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                                                                          200
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                                                                                                                                      /dev_stage="Meiotic stages pre-meiosis-metaphase I"
/lab_host="E. coli DH10B"
/clone_lib="Wheat meiotic anther cDNA library"
/clone_lib="Wheat meiotic anther cDNA library"
/clone_lib="Wheat meiotic anther cDNA library"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Plants
/note="Vector: pSPORT1 by Tim Sutton in the Plangridge Lab at the
psportion of plant Science, University of Adelaide, Waite
Campus, Australia. Average insert size 1.5Kb. Plasmid DNA
/note="Vector: pSPORT1 by Tim Sutton in the Plangridge Lab at the
paration and DNA recrease insert size 1.5Kb. Plasmid DNA
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                                                                          preparations and DNA sequencing were performed in the Anderson lab (all other authors)."  119 \ c \qquad 164 \ g \qquad 113 \ t 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4565"
/clone="WHE4018_D05_G10"
/tissue_type="Anther"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Triticum aestivum"
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94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
    86.3%;
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    Score 16.4;
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  DB 14;
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A1496684
602 bp mRNA linear EST 07-JU
fb48e09.yl Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3715144 5' similar to SW:IAP_CHICK Q90660 INHIBITOR OF
APOPTOSIS PROTEIN ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i (bases 1 to 602)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Bddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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High quality sequence stop: 482
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Stephen L. Johnson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity on wrong strand
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Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                          stage embryos"
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                                                                                                                                                                                                                                                                                                                                              tissue_type="26 somite embryos, adult livers, shield"
                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7955"
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0; Mismatches 1
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The library was constructed by Dr. Z. Gong. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis. Plea contact Zhiyuan Gong for further information on this library (National University of Singapore, Department of Biological Sciences, Lower Kent Ridge Road, Singapore 119260).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 627)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwoo, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: fz24f09.y1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ074707 627 bp mRNA linear EST 02-APR-2 fz24f09.x1 Gong zebrafish testis Danio rerio cDNA 3' similar to SW:IAP_CHICK Q90660 INHIBITOR OF APOPTOSIS PROTEIN ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 473.
Location/Qualifiers
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BQ074707.1
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Unpublished
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                                                                                        /lab_host="DH108 (phage-resistant)"
/clone_lib="Gong zebrafish testis"
/note="Organ: testis (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the testes of 31 male adult zebrafish (4-5 month old).
CDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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(http://genome.wustl.edu/est/lambda_protocol.shtml). Please contact Zhiyuan Gong for further information this library (National University of Singapore,
                                                                            University protocol
                                                                                                                                                                                                                                                                                                                                                                          organism="Danio rerio"
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Ning Wu. cDNA Library Arrayed by:
Research Genetics. DNA Sequencing by: Washington University
Sequencing Center Clone distribution: Research Genetics web
address: http://www.researchgenetics.com/
Seq primer: T3 ET from Amersham
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy ,S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Kohler, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE557791 672 bp mRNA linear EST 30-AUG-
fllog10.yl Zebrafish Research Genetics C32 fin Danio rerio cDNA
similar to SW:IAP2_HUMAN Q13490 INHIBITOR OF APOPTOSIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE557791.1
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                                                                                    /clone lib="Zebrafish Research Genetics C32 fin"
/note="Vector: pT7T3D-Pac with a modified polylinker;
Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was prepared from zebrafish(C32) fin, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is non-normalized. Library was constructed by Ning Wu. NOTE: This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info.llnl.gov)for further information"

59 a 181 c 127 g 205 t
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a 156 c 119 g 203 t
                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:7955"
/tissue_type="Fin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Danio rerio"
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94.4%;
 86.3%;
94.4%;
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Score 16.4; DB 10;
Pred. No. 3e+03;
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Pred. No. 2.9e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MO 63108,
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Minimum
Maximum
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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     0000000000000000
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                                                                                                                                                                                                                Score
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                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq: *
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq: *
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq: *
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq: *
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                591
1068
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11193
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3426
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6/ptodata/2/pubpna/US08
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                                                                                                                                                                                                               BB
                   3 US-10-029-386-9548

0 US-09-922-895-2

3 US-10-276-950-2

3 US-09-826-509-474

6 US-10-293-050-6

0 US-10-283-028-5

3 US-10-283-028-3

3 US-10-225-567A-63

0 US-09-931-381A-15

3 US-10-283-028-1

0 US-09-964-824A-100

4 US-10-106-623-3

4 US-10-001-835-29

US-09-864-761-9611
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Sequence 9548, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 474, App
Sequence 6, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 15, Appl
Sequence 100, App
Sequence 29, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 9611, Ap
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113 14 14	4 2 2 2 2 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4	1133 1133 1134 1133 1133 1133 1133 1133
US-10-027-632-262488 US-10-027-632-262489 US-10-027-632-262489 US-10-027-632-262488	-10-027-632-2813 -10-027-632-8134 -10-027-632-1097 -10-027-632-3018 -10-027-632-3018 -10-027-632-3018 -10-027-632-8134 -10-027-632-8134 -10-027-632-1097 -10-027-632-1097 -10-027-632-3018	-09-745-605-2 -10-027-632-13644 -10-027-632-16561 -10-027-632-16561 -10-027-632-16561 -10-188-619-14 -10-198-613-447 -10-999-926-583 -10-099-926-583 -10-027-632-28156 -10-027-632-28156
Sequence 301813, Sequence 262488, Sequence 262489, Sequence 262488,		

ALIGNMENTS

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US-10-029-386-9548/c
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AEOMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386 CURRENT FILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 9548
                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9548, Application US/10029386 Publication No. US20030194704A1
                                                                                    Matches
                                                                                                                                                                                                           OTHER INFORMATION: MAP TO CHR3.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8

OTHER INFORMATION: WILSPROT HIT: P51677, EVALUE 1.00e-102

OTHER INFORMATION: EXT_HUMAN HIT: BG182330.1, EVALUE 0.00e+00

OTHER INFORMATION: EST_HUMAN HIT: BG182330.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 591
                                                                                                              Local
1 CTGGGCCATCAGTGCTCTG 19
                                                                                    l Similarity
19; Conserv
                                                                             100.0%; Score 19; Dilarity 100.0%; Pred. No. 3.: Conservative 0; Mismatches
                                                                                                                                    DB 13; Length 591;
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                                                                                    Indels
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                                                                                    Gaps
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CTGGGCCATCAGTGCTCTG 41

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TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-922-895-2
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US-09-922-895-2/c
                                                                                                                                                                             US-10-276-950-2/c
                                                     Sequence 2, Application US/10276950
Publication No. US20030157639A1
GENERAL INFORMATION:
APPLICANT: GLAXO GROUP LIMITED
TITLE OF INVENTION: PROTEIN AND ASSAY
FILE REFERENCE: PG3810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09922895 Publication No. US20020192214A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                           Matches
PRIOR APPLICATION NUMBER: GB 0013345.4
                 CURRENT APPLICATION NUMBER: US/10/276,950 CURRENT FILING DATE: 2002-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,895
FILING DATE: 06-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/847,296
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/017,113
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,382
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SICILIANO, SALVATORE J.

SPRINGER, MARTIN J.

TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
                                                                                                                                                                                                                                                             105
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STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 908-594-3904
TELEFAX: 908-594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 07065-0900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Thies,
                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 3.2;
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; LENGTH: 1068
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1068)
US-10-276-950-2
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US-10-293-050-6/c
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                                                                                                                                                                                                                                  Sequence 6, Application US/10293050 Publication No. US20030130494A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local
                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liaw, Chen W.
APPLICANT: Lin, I-Lin
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known (
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
APPLICANT: Wang, Wei
APPLICANT: Yoshimura, Akihiko
TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS
FILE REFERENCE: DX0506B US
CURRENT APPLICATION NUMBER: US/10/293,050
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: US 08/567,882
PRIOR FILING DATE: 1995-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                              APPLICANT: Dairaghi, Daniel J. APPLICANT: Hara, Takahiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1068
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lehmann-Bruinsma, Karin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 100.0%; Score 19; DB 13; Local Similarity 100.0%; Pred. No. 3.2;
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l Similarity 100.0%;
19; Conservative 0
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                                                                                                                                                          Miyajima, Atsushi
Schall, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09826509 o. US20030204073A1
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NUMBER OF SEQ ID NOS: 9

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RESULT 6
US-10-283-028-5/c
; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-283-028-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/10283028 Publication No. US20030143684A1
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NAME/KEY: CDS
LOCATION: (1)..(1071)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 
SEQ ID NO 6
                                                                                                       TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/283,028
FILING DATE: 28-Oct-2002
CLASSIFICATION - CUnknown>
PRIOR APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LK:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND ANTAGONISTS THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGCCATCAGTGCTCTG 87
                                   TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Militia Drive
                                                                                           LENGTH: 1116 base pairs
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                                                                Best Loc
Matches
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                                                                                                                                                                                                                                                                                                     TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/720,565

FILING DATE: 30-SEP-1996
APPLICATION NUMBER: PCT/US96/00608

FILING DATE: 19-JAN-1996
APPLICATION NUMBER: US 08/375,199

FILING DATE: 19-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: LKS94-05A2

TELECOMMUNICATION: 117-861-6240
                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                  NAME/KEY: CDS
LOCATION: 92..1156
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE ANTAGONISTS THEREOF
                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gerard, Craig J.
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196 CTGGGCCATCAGTGCTCTG 178
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                                                                                Similarity
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                                CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                       LENGTH: 1193 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGCCATCAGTGCTCTG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/283,028 FILING DATE: 28-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Lexington STATE: MA
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                                                                 Conservative
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                                                                                                                                                                                                                                       linear
                                                              100.0%; Score 19; DB:
100.0%; Pred. No. 3.2;
tive 0; Mismatches
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100.0%; Pred. No. 3.2;
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                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -09-931-381A-15/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 1855.2010-003
CURRENT APPLICATION NUMBER: US/09/931,381A
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: U.S. 09/638,914
PRIOR FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atent No.
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pan, Junliang
APPLICANT: Soler-Ferran, Dulce
TITLE OF INVENTION: Method for Identifying Agents Which
TITLE OF INVENTION: Modulate Chemokine "MEC"-Induced Functions of CCR3 and/or
TITLE OF INVENTION: CCR10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       equence 15, Application US/09931381A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-225-567A-63/c
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ORGANISM: Homo sapiens
                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (181)...(124)
NAME/KEY: misc_feature
LOCATION: (1291)...(12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: Butcher,
                                                                                                                                                                LOCATION: (129\overline{1})...(1291)
OTHER INFORMATION: n = A,
                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 1201
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1 Similarity 100.0%;
19; Conservative (
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                                                                                           Similarity
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                                    creeeccarcaerecrere 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kunkel, Eric J.
                                                                        Conservative
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                                                                                                                                                                                                                    (1248)
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                                                                       100.0%; Score 19; DB
100.0%; Pred. No. 3.2;
tive 0; Mismatches
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                                                                                                                                                                 C or
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Pred. No. 3
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                                                                                                           DB 10;
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                                                                       0;
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                                                                                                          Length 1689;
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                                                                       Gaps
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; TOPOLOGY: linear;; woudle
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-283-028-1
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                                         US-09-964-824A-100/c
                                                            RESULT 11
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Sequence 100, Application US/09964824A Patent No. US20020102531A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10283028 Publication No. US20030143684A1 GENERAL INFORMATION:
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                   Query Match .
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <Unknown>
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: US/08/720,565
FILING DATE: 30-SEP-1996
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,028
FILING DATE: 28-Oct-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND
                                                                                                                       285 CTGGGCCATCAGTGCTCTG 267
                                                                                                                                                                                                   19;
                                                                                                                                                             CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1689 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 617-861-6240
                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerard, Craig J.
Gerard, No. US20030143684Alma P.
Mackay, Charles R.
Ponath, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Theodore W.
                                                                                                                                                                                                   0;
                                                                                                                                                                                                   Score 19; DB
Pred. No. 3.2
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKS94-05A2
                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                      Length 1689;
                                                                                                                                                                                                    0;
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                    0;
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GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73

Determination and Therapeutic Screening Using Signatus

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RESULT 12
US-10-106-623-3/c
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; LENGTH: 1717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/771,276
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20020150888Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33670
TELEPHONE: 312-474-6300
TELEPHONE: 312-474-6300
TELEPAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10106623 Publication No. US20020150888A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raport, Carol J. TITLE OF INVENTION: Chemokine Receptor Materials and Methods
                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gray, Patrick W.
                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois COUNTRY: USA
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/106,623 FILING DATE: 26-Mar-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
                                                                             NAME/KEY:
                                                    LOCATION:
                                                                                                                                                                                                                LENGTH: 1915 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF SEQUENCES:
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                                                  CDS
362..1426
                                                                                                                                                linear
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   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vicky L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-10-04

PRIOR PILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/001,835
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,997
PRIOR FILING DATE: 2000-11-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Prot
FILE REFERENCE: DEX-0277
FILE REFERENCE: DEX-0277
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3426
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 CTGGGCCATCAGTGCTCTG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 CTGGGCCATCAGTGCTCTG 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3426
PLICATION NUMBER: PCT/US01/00666
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Cafferkey, Robert
Sun, Yongming
Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10001835
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100.0%; Pr
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100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19; DB Pred. No. 3.2 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 9611

LENGTH: 549

TYPE: DNA

COCANICAL TIMES AND THE SECONDOWN AND THE SECON
                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXC.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 152
LENGTH: 563
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-029-386-152/c
; Sequence 152, Appl:
; Publication No. US;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-864-761-9611
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
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OTHER INFORMATION: MAP TO CHR22_83.0
                                        FEATURE:
                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R INFORMATION:
R INFORMATION:
R INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10029386 o. US20030194704A1
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N: EXPRESSED IN PLACENTA, SIGNAL = 1.7

N: EXPRESSED IN HELA, SIGNAL = 1.4

N: EXPRESSED IN HEART, SIGNAL = 1.9

N: EXPRESSED IN LUNG, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

N: EXPRESSED IN ADULT LIVER, SIGNAL = 4.6

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6

N: EXPRESSED IN BRAIN, SIGNAL = 1.5
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94.7%;
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Pred. No. 22;
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; LENGTH: 1516
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-745-605-2
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                       PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: 1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 136447, Application US/10027632 Publication No. US20030204075A9
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Best Local Similarity
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OTHER INFORMATION: N
OTHER INFORMATION: S
OTHER INFORMATION: S
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APPLICANT: Finger, Joshua N.
TITLE OF INVENTION: NOVEL IMMUNOGLOBIN SUI
TITLE OF INVENTION: AND APEX-3 AND USES 7
FILE REFERENCE: DB13NP
CURRENT APPLICATION NUMBER: US/09/745,605
CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 44
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OTHER
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N: EXPRESSED IN LUNG, SIGNAL = 1.7

N: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2

N: EXPRESSED IN HELA, SIGNAL = 6.2

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

N: EXPRESSED IN HEART, SIGNAL = 1.6

N: EXPRESSED IN HEART, SIGNAL = 1.6

N: EXPRESSED IN BRAIN, SIGNAL = 1.6

N: EXPRESSED IN HEART, SIGNAL = 1
NUMBER: US 60/167,363
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94.7%;
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Pred. No. 22;
O; Mismatches
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Pred. No. 2
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US-10-027-632-136447
; Sequence 136447, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; FILE REFERENCE: 108827.129
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,368
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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US-10-027-632-165611
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                                                                                                                                                                                            RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Human US-10-027-632-165611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 165611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 165611, Application US/10027632 Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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PRIOR APPLICATION NUMBER: US 60/156,358
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 82
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                 16; Conservative
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100.0%; Pred. No. 1.
tive 0; Mismatches
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. 1.2e+02;
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hes 0;
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Sequence 165611, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
pRIOR FILING DATE: 2000-07-12
pRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR APPLICATION NUMBER: US 60/167,363
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-28
PRIOR FILING DATE: 1999-08-09
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 136447
LENGTH: 824
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 824
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16; Conserv
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100.0%; Pred. No.
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RESULT 22
US-09-747-377-447/c
; Sequence 447, Application US/09747377
; Publication No. US20030022255A1
; GENERAL INFORMATION:
APPLICANT: Morris, David
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER
FILE REFERENCE: A-69959/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/747,377
; CURRENT FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 493
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 447
LENGTH: 145
TYPE: DNA
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Best Local (
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Publication No. US20030162944A1
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APPLICANT: Christ
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4474
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TYPE: DNA ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/188,619
FILING DATE:
CTACCTTON
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ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING
TITLE OF INVENTION: SPECIFIC COMPOUNDS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL:
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CITY: New York
STATE: New York
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17; Conserv
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1185 Avenue of the Americas
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Pred. No. 1.
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2;
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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 583
RESULT 25
US-10-099-926-583
; Sequence 583, Application US/10099926
; Publication No. US20030166064A1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-583
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US-09-920-300A-583
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APPLICANT: MOTTIS, David

APPLICANT: MOTTIS, David

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR BREAST CANCER

FILE REFERENCE: A-69959/RMS/DCF

CURRENT APPLICATION NUMBER: US/10/105,613

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: US/09/747,377

PRIOR PILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 49-3

NUMBER OF SEQ ID NOS: 49-3

NUMBER OF SEQ ID NOS: 49-3
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Best Local (
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TYPE: DNA
ORGANISM: Mus sp.
                                                                                                                                                                                                      Local
                                                                                                                                                                              83.2%;
1 Similarity 89.5%;
17; Conservation
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                                                                                                              CTGGGCCATGACTGCTCTG 255
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o. US20030099963A1
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                                                                                                                                                                                      Score 15.8; DB 10;
Pred. No. 1.5e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15.8; DB 15
Pred. No. 1.5e+02;
0; Mismatches 2
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                         Length 422;
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GENERAL INFORMATION:

APPLICANT: King, APPLICANT: Meagl

Meagher, Madeleine

Joy

Gordon E

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APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 583
LENGTH: 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C2
CURRENT APPLICATION NUMBER: US/10/099,926
CURRENT FILING DATE: 2002-03-17
NUMBER OF SEQ ID NOS: 1982
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 583
LENGTH: 422
TYPE: DNA
ORGANISM: Homo sapiens
US-10-099-926-583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-583
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US-10-033-528-583
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US-10-027-632-281562/c
Sequence 281562, Application US/10027632
Publication No. US20030204075A9

GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 583, Application US/10033528
Publication No. US20020131971A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Secrist, Heat
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                     237 CTGGGCCATGACTGCTCTG 255
                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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89.5%;
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Pred. No. 1.
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Pred. No. 1.
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,363
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-09-08-09
PRIOR FILING DATE: 1999-08-09
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US-10-027-632-281563/c
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PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 281563, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                        Matches
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Best Local
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LENGTH: 492
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 325720 SOFTWARE: FastSEQ for Windows Version 4.0
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17; Conserv
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CTGGGCCATGACTGCTCTG 364
                                                                                          Conservative
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                                                                                                              83.2%;
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Pred. No. 1.5e
0; Mismatches
                                                                                                                Score 15.8;
Pred. No. 1
                                                                                          Mismatches
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                                                                                                                                  DB 13;
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                                                                                          Gaps
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RESULT 29 US-10-027-632-281562/c ; Sequence 281562, Application US/10027632

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PRIOR APPLICATION NUMBER: US 60/198,676;
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483;
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 281562
                                                                                                                                NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 281563
LENGTH: 492
TYPE: DNA
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Best Local Similarity
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                                         Query Match
                                                                                     ORGANISM: Human
-10-027-632-281563
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-10-027-632-281562
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 108827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 492
 Local Similarity 89.1
1es 17; Conservative
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                       83.2%;
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Score 15.8; DB 14;
Pred. No. 1.5e+02;
0; Mismatches 2;
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Pred. No. 1.
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                                          DB 14;
                                            Length 492;
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     Indels
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     Gaps
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
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US-10-027-632-81347
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-19-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 81347, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 652

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(652)

OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339
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Pred. No. 1.5e
0; Mismatches
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Sequence 109771, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; TITLE OF INVENTION NUMBER: US/10/027,632

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR FILING DATE: 2000-04-20

; PRIOR FILING DATE: 2000-03-29

; PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109771
LENGTH: 652
RESULT 34
US-10-027-632-109772
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81347
LENGTH: 652
                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                             FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(652)

OTHER INFORMATION: n = A,T,C or G
-10-027-632-109771
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(652)
OTHER INFORMATION: n = A,T,C
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                                                                                                                                                                            Local
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17; Conserv
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17; Conserv
                                                                               CAGGGCCATCAGGGCTCTG
                                                                                                                    CTGGGCCATCAGTGCTCTG 19
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                                                                                                                                                            Conservative
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89.5%;
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                                                                               357
                                                                                                                                                                              Score 15.8;
Pred. No. 1.
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Pred. No. 1.5e+02;
D; Mismatches 2;
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                                                                                                                                                                              .5e+02
                                                                                                                                                                                                   DB 13;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827:129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 301812
LENGTH: 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C
US-10-027-632-109772
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
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Best Local Similarity
Matches 17; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(652)
OTHER INFORMATION: n = A,T,C or G
US-10-027-632-301812
                                                                                                                                                                RESULT 37
US-10-027-632-81346
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Best Local Similarity 89.5
Matches 17; Conservative
Sequence 81346, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(652)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/156,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                              83.2%;
Local Similarity 89.5%;
es 17; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE: 1999-11-23
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89.5%;
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                              Score 15.8;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                   Length 652;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or
US-10-027-632-81346
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                                                      i NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-81347
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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Query Match
Best Local Similarity
                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human
                                                                                                                                TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                        ENGTH: 652
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 Score 15.8; DB 14;
Pred. No. 1.5e+02;
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23
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; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-109771
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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US-10-027-632-109772
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109771
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GENERAL INFORMATION:
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; LENGTH: 652
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(652)
; OTHER INFORMATION: n = A,T,C or
US-10-027-632-109772
Search completed: January 13, 2004, 21:03:12 Job time : 127.5 secs
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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                                                                                 GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-08-847-2968-2
US-08-567-882-6
US-08-720-565-3
US-08-720-565-1
US-08-720-565-1
US-08-720-565-1
US-08-720-565-1
US-08-720-565-1
US-08-687-355A-14
US-09-407-367-14
US-09-016-434-1062
US-08-687-355A-1
US-09-015-296-2
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3 US-09-168-629-14
3 US-09-215-131-1
3 US-09-222-734-1
3 US-09-235A-13
4 US-09-465-901-15
US-09-465-901-35.
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                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible.

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/847,296B

FILING DATE: 24-APR-1997

CLASSIFICATION E 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/016,158

APPLICATION NUMBER: 60/017,113

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 60/017,113

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 50/017,113

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 35,382

REFERENCE/DOCKET NUMBER: 19634Y

TELEPHONE: 908-594-3904

TELEPAX: 908-594-4720
       Query Match
                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DAUGHERTY, BRUCE L.
APPLICANT: DEMARTINO, JULIE A.
APPLICANT: SICILIANO, SALVATORE J.
APPLICANT: SPRINGER, MARTIN J.
TITLE OF INVENTION: EOSINOPHIL EOTAXIN RECEPTOR
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
STATE: NJ
COUNTRY: USA
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US-09-685-462-9
US-09-581-831-1
US-09-620-312D-688
US-08-311-731A-132
US-08-742-023-15
US-08-968-505-15
US-09-016-434-481
US-09-404-879A-327
US-09-404-879A-327
US-09-461-697-114
US-09-461-697-114
US-09-461-697-104
US-09-461-697-104
US-09-461-697-100
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Length 1065;

Minimum DB Maximum DB

Title: Perfect score:

Sequence:

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US-08-720-565-5/c
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                                                                                                                                                                                                                                                                                    US-08-567-882-6
                                           Sequence 5, Application US/08720565 Patent No. 6537764 GENERAL INFORMATION:
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08567882 Patent No. 6512103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Pred. No. 0.87; Matches 19; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1071 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/567,882 FILING DATE: 08-DEC-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1071 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                         105 CTGGGCCATCAGTGCTCTG 87
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Gerard,
Gerard,
Mackay,
                                                                                                                                                                                                                      Conservative
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1..1071
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/ENTION: MAMMALIAN CHEMOKINE REAGENTS
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                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  jhi, Daniel J.
Takahiko
 No. 653776
Charles R.
               Craig J.
No. 6537764ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas J.
                                                                                                                                                                                                                                    100.0%; Score 19; DB 4
100.0%; Pred. No. 0.87;
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US-08-720-565-3/c
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Best Local S
Matches 19
                                                                                                                                  sequence 3, Application US/08720565
Patent No. 6537764
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
BILING DATE: 19-JAN-1995
                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
             TITLE OF INVENTION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                       Post,
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                                             Qin, Shixin
                                                                           Ponath,
                                                                                         Mackay,
                                                                                                          Gerard,
                                                                                                                          Gerard,
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                                                           Theodore W.
                                                                             Paul D
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           G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND ANTAGONISTS THEREOF
                                                                                         No. 6537764ma
Charles R.
                                                                                                                         Craig J.
                                                                                                                                                                                                                                                                                                                100.0%; Score 19; DB 4
100.0%; Pred. No. 0.88;
tive 0; Mismatches
18
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CORRESPONDENCE ADDRESS:

CITY: Le STATE: N COUNTRY:

Lexington MA

TRY: USA 02173 STREET:

ADDRESSEE:

E: Hamilton, Brook, Smith & Reynolds, Two Militia Drive

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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; LOCATION:
US-08-720-565-3
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Best Local Similarity
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FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00608
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375,199
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: LKS94-05A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 61-6240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1193 base pairs
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
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                                                       PRIOR APPLICATION DATA:
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STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                        APPLICATION NUMBER: FILING DATE: HEREW CLASSIFICATION:
                                                                                                                                                                                                                                                                                         ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                        UNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 CTGGGCCATCAGTGCTCTG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1085, Application US/09016434
5. 6500938
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; CLONE: g1199579
US-09-016-434-1085
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TELEFAX: 617-861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                    FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,9
REFERENCE/DOCKET NUMBER:
                                                                                                                                                          APPLICATION NUMBER: PCT/I
FILING DATE: 19-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 19-JAN-1995
                                                                                                                                                                                                                                                CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTOR GENE CCR3 AND TITLE OF INVENTION: ANTAGONISTS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 100.0%; Score 19; DB 4
Local Similarity 100.0%; Pred. No. 0.89;
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 30-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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5. 6537764
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Teth, Paul D.
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Two Militia Drive
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No. 6537764ma P.
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                                                                                        LKS94-05A2
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RESULT 8
US-08-687-355A-14/c
; Sequence 14, Application US/08687355A
                                                                                                                                                                                                            ; NAME/KEY: misc_feature; OTHER INFORMATION: /= "88-2B polynucleotide and amino acidus-08-575-967A-3
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TELEFAX: 206-485-1662
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6265184and, Greta
NAME: NO. 8265184and, Greta
NAME: NO. 8265184and, Greta
NAME: NO. 8265184and, Greta
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/575,967A
FILING DATE:
                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 206-485-1900
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: cDNA
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Local Similarity 100.0%; Pred. No.
nes 19; Conservative 0; Mismatch
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STRANDEDNESS:
                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                   LOCATION:
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gDNESS: double
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ower, 233 S. Wacker Drive
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                                                                                                                                                                     Score 19; DB 3; Pred. No. 0.94;
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                                                                                                                                                                                                                                                                               Sequence 14, Application US/09407367
Patent No. 6420532
GENERAL INFORMATION:
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APPLICANT: Synaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44'
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                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                        STREET: III.
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TYPE: nucleic acid
STRANDEDNESS: single
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APPLICATION NUMBER: FILING DATE:
                                                                                                                                          COUNTRY: U.S.A.
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RY: U.S.A.
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1185 Avenue of the
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                                                                                                                                                                                                                                       Christophe P.G. Gerald, et al. VENTION: METHOD OF OBTAINING CEQUENCES: 27
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Pred. No. 25;
0; Mismatches
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RESULT 10
US-09-016-434-1062
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US-09-407-367-14
                                                                                      CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1062:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1062, App
Patent No. 6500938
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Best Local (
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                       CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
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TOPOLOGY: line
MMEDIATE SOURCE:
LIBRARY: GENBA
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TELEPHONE: 212-391-0525
TO NO:
                                             STRANDEDNESS:
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REFERENCE/DOCKET NUMBER:
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DEDNESS: single
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FR: 28,678
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Pred. No. 2
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US-08-687-355A-1
; Sequence 1, Application US/08687355A
; Patent No. 5989834
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| Best Local
                                          RESULT 12
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US-08-192-288-1
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                                                                                                                                         Matches
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/192,288

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44742/JPW/TEP

TELEPHONE: (212) 97-9550

TELEPHONE: (212) 97-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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NAME/KEY:
LOCATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: cDNA
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TITLE OF INVENTION: DNA ENCODING
TITLE OF INVENTION: Y/PEPTIDE YY
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                        Local Similarity
les 17; Conserv
                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                   558
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                                                                                                   1 CTGGGCCATCAGTGCTCTG 19
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5545549
                                                                                                                                                                                                                                                                                           nucleic acid
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Walker,
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43..1185
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Pred. No. 39;
0; Mismatches
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Pred. No. 39;
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                                                                                                                                                                  Length 1280;
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; NAME/KEY:
; LOCATION:
US-08-687-355A-1
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Best Local Similarity
Matches 17; Conserv
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,355A

FILING DATE: NO.5.998934ember 26, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44742-A-PCT/JPW/MAT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Appli
Patent No. 642053
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Christ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                              TITLE OF INVENTION: ME NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                   STREET: 1185 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Synaptic Pharmaceutical Corporation
ITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
ITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                       ZIP: 10036
                                                                                                                                                                     COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : LOPOTOGA
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ilarity 89.5%;
Conservative
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VENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPO
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                US/09/407,367
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Pred. No. 39;
0; Mismatches
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FEATURE:
NAME/KEY:
LOCATION:
US-09-407-367-1
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Best Local Similarity
Thes 17; Conserv
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                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,296
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                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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MMEDIATE SOURCE
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 28 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                              TELEFAX: 650-845-4166
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                       STRANDEDNESS:
                                       TYPE: nucleic acid
                                                      ENGTH:
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3174 Porter Drive
                                                      1786 base pairs
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ER: 28,678
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Pred. No. 39;
0; Mismatches
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LIBRARY: LUNGTUT12; CLONE: 3128715; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-593-722-2
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US-09-593-722-2/c
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Best Local Similarity 89.5%;
                                                             Matches
                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/015,296
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0467
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: 3128715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: HUMAN BETA-ALANINE-PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1270
1270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
                                                             17;
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                                                                            Similarity
                            CTGGGCCATCAGTGCTCTG 19
CAGGGCCATCAGTGCTCAG 1252
                                                                                                                                                                                                                LENGTH: 1786 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGGCCATCAGTGCTCAG 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-Jun-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/593,722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94304
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                                                                                                                                                                                                                                                                                                                   650-845-4166
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                                                                          83.2%;
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                                                           Score 15.8; D
Pred. No. 41;
0; Mismatches
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Pred. No. 4:
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RESULT 16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Baez,
APPLICANT: Yang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (317)276-2763
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                               quence 3, Application US/08876798A
tent No. 6355478
                                                                                                                             APPLICANT: BAEZ, MEIVYN
APPLICANT: YANG, PEIYI
APPLICANT: YANG, PEIYI
TITLE OF INVENTION: RHESUS MONKEY NEUROPEPTIDE Y RECEPTOR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-JUN-199
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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TELECOMMUNICATION INFORMATION:
                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: RHESUS MONKEY NEUROPEPTIDE Y RECEPTOR NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                               578 CTGGGGCATCAGTGCCCTG 596
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                                                                                    46285
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                                                                                                Indiana
Y: U.S.A.
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63..1205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Pred. No. 42;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-311-731A-1
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (317)276-2763
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equence 1, Application US/08311731A
htent No. 6583266
                                                                                                                                            TELEFAX: 617/720-2441
[NFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENERAL INFORMATION:
            MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: ci-
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
NUMBER OF SEQUENCES: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2144 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
DRIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 2144 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: BOSTON
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al Similarity 68.4%;
13; Conservative
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                                                    DNA (genomic)
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Pred. No. 42
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Query Match
Best Local Similarity
Watches 16; Conserva
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US-09-103-840A-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-103-840A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-103-840A-2
                                                                            US-09-103-840A-1
                                                                                                                                                                 SOFTWARE:
SEQ ID NO 1
Query Match 81.1%; Score 15.4; I Best Local Similarity 94.1%; Pred. No. 84; Matches 16; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09103840A Patent No. 6294328
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                      FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M.
                                                                                                                                                                                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                               LENGTH: 44
TYPE: DNA
                                                                                           ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 4403765
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Similarity 94.1%;
                                                                                                                                                                                  PatentIn Ver. 2.1
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94.1%;
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Pred. No. 97;
0; Mismatches
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                                         DB 3;
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                                       Length 4411529;
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RESULT 22
US-09-215-131-1/c
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RESULT 23
US-09-222-734-1/c
; Sequence 1, Application US/09222734A
                                                                                                                                                                                                                                          US-09-215-131-1
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; NAME/KEY: CDS
; LOCATION: (36)..(2306)
US-09-168-629-14
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Best Local Similarity 100.
Marches 15; Conservative
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Chu, Keting
APPLICANT: Pot, David

TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
FILE REFERENCE: 1449.002
CURRENT APPLICATION NUMBER: US/09/215,131
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3966
TYPE: DATE: 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 14, Application US/09168629 Patent No. 6242253
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                                                                                                                                                                     Matches
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LENGTH: 2931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Karin, Michael
APPLICANT: DiDonato, Joseph A.
APPLICANT: DiDonato, Joseph A.
APPLICANT: Rothwarf, David M.
APPLICANT: Hayakawa, Makio
APPLICANT: Zandi, Ebrahio
APPLICANT: Zandi, Ebrahio
TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
FILE REFERENCE: P-UD 3295
CURRENT APPLICATION NUMBER: US/09/168,629
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 60/061,470
EARLIER FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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mes 15; Conserv
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100.0%; Pred. No.
ive 0; Mismatches
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. 1.1e+02;
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US-08-687-355A-13
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Best Local Similarity
Query Match
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APPLICANT: Pot, David
TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
FILE REFERENCE: 12441.78080
CURRENT APPLICATION NUMBER: US/09/222,734A
CURRENT FILING DATE: 1998-12-29
EARLIER APPLICATION NUMBER: 09/215,131
EARLIER APPLICATION NUMBER: 09/215,131
EARLIER APPLICATION NUMBER: 60/068,954
                                                                                                                                                                                             TELEPHONE: 212-278-040
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4474
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-12-30 NUMBER OF SEQ ID NOS: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 3966
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,355A
FILING DATE: No. 5989834ember 26, 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                         MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Synaptic Pharmaceutical Corporation
TITLE OF INVENTION: NUCLEIC ACID ENCODING NEUROPEPTIDE
TITLE OF INVENTION: Y/PEPTIDE YY (Y2) RECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                       STRANDEDNESS:
                                                                                                                     TOPOLOGY:
                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2433 CTGGGCCATCAGTGC 2419
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                                                                                                                                   H: 45 base pairs nucleic acid DEDNESS: single
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                                                                                                                     linear
                                                                                              (genomic)
 77.98;
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 Score 14.8;
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1.2e+02;
   DB
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 Length 45;
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TELECUPATION: 214 TELEPHONE: 212-391-0525
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
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Sequence 13, App
No. 64205
                                                                                                                                                    Sequence 15, Application US/09465901 Patent No. 6492143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Matches 16; Conserv
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-09-465-901-15
APPLICANT: Reed, Randall
APPLICANT: Yau, King-Wai
APPLICANT: Yau, King-Wai
APPLICANT: Krautwurst, Dietmar
TITLE OF INVENTION: Olfactory Receptor Expession Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,367
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Christ
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MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
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STREET: New York
STATE: New York
TOWNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Christophe P.G. Gerald, et al.
TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2 SPECIFIC COMPONUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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1185 Avenue of the Americas
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Pred. No. 80;
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APPLICANT: Zon, Leonard I.
APPLICANT: Agarwal, Sadhana
APPLICANT: Best, Jennifer
APPLICANT: Best, Jennifer
APPLICANT: Vail, Brenda
ITITLE OF INVENTION: Two Sterile-20 Kinase-Like Proteins and
ITITLE OF INVENTION: Methods of Use Thereof
ITITLE OF INVENTION NUMBER: US/09/685,462
CURRENT APPLICATION NUMBER: US/09/685,462
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/591,083
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US98/26116
PRIOR APPLICATION NUMBER: US 60/069,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: PCR primer
US-09-465-901-35
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US-09-685-462-1/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 669
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Olfactory Receptor Expession Libraries TITLE OF INVENTION: ad Methods of Making and Using Them FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: US/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR FILING DATE: 1998-12-17
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NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Randall APPLICANT: Yau, King-Wai APPLICANT: Krautwurst, Dietmar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
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al Similarity 88.9%;
16; Conservation
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11 Similarity 88.9%;
16; Conservation
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Pred. No. 1
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Pred: No. 1
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1.2e+02;
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APPLICANT: Agarwal, Sadhana
APPLICANT: Best, Jennifer
APPLICANT: Vail, Brenda
TITLE OF INVENTION: Two Sterile-20 Kinase-Like Proteins and
TITLE OF INVENTION: Methods of Use Thereof
FILE REFERENCE: 1242.1016-004
CURRENT APPLICATION NUMBER: US/09/685,462
CURRENT FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 09/591,083
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: PCT/US98/26116
PRIOR APPLICATION NUMBER: PCT/US98/26116
PRIOR APPLICATION NUMBER: US 60/069,078
PRIOR APPLICATION NUMBER: US 60/069,078
PRIOR APPLICATION NUMBER: US 60/069,078
PRIOR FILING DATE: 1997-12-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (20)...(1258)
US-09-685-462-1
                                                                                                                                                                                            US-09-581-831-1
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                                                                                                                                Sequence 1, Application US/09581831 Patent No. 6448020 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                Query Match 777.9
Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9%;
Matches 16; Conservative
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                    APPLICANT: TOPTGARD, RUNE APPLICANT: ZAPHIROPOULOS, E APPLICANT: KOGERMAN, PRIIT APPLICANT: GRIMM, THOMAS
              APPLICANT: GRIMM, THOMAS TITLE OF INVENTION: MOLE TITLE OF INVENTION: GENE
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 9, Application US/09685462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
FEATURE:
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMATION:
PPLICANT: Zon, Leonard I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1294 TGGGCCTTCAGTGCGCTG 1277
                                                                                                                                                                                                                                                                             1604 TGGGCCTTCAGTGCGCTG 1587
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                                                                                                                                                                                                                                                                                                           TGGGCCATCAGTGCTCTG 19
50695-60568
              MOLECULES ASSOCIATED WITH THE HUMAN SUPPRESSOR OF FUSED GENE
                                                                                                                                                                                                                                                                                                                                                                            77.9%;
                                                                                              PETER G.
                                                                                                                                                                                                                                                                                                                                                                          Score 14.8; DB 4;
Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               Length 1744;
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (169)..(1134)
US-09-620-312D-688
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                                                                                                                                                              NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 688
LENGTH: 2529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
SEQ ID NO 1
 Query Match 77.9%;
Best Local Similarity 88.9%;
Matches 16; Conservative
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8 No. 6569667
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                                                                                                                                                                                                                                       APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/581,831
CURRENT FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCT/SE98/02383
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 9704788-0
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 9802293-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (167)..(1618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICAN'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2239
TYPE: DNA
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Similarity 88.9%;
16; Conservative
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09620312D
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idi, Vinod
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; Score 14.8; DI
; Pred. No. 1.4e-
0; Mismatches
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Pred. No. 1
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  8; DB 4;
1.4e+02;
ches 2;
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                               Length 2529;
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   Indels
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   0
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   Gape
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CTGGGCCATCAGTGCTCT

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US-08-311-731A-132/c
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                                   Patent No. 5800997

GENERAL INFORMATION:

APPLICANT: Beck, James J.

TITLE OF INVENTION: Detection of Maize Fungal Pathogens
TITLE OF INVENTION: Using the Polymerase Chain Reaction
                                                                                                                               Sequence 15, Application US/08742023 Patent No. 5800997
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                          Query Match
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GENERAL INFORMATION:
                                                                                                                                                                   08-742-023-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 36412 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MYCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (of HYPOTHETICA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 411
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: COO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                           77.9%;
Local Similarity 88.9%;
les 16; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/311,731A FILING DATE: CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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     DDRESSEE
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: MASSACHUSETTS
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                                                                                                                                                                                                                                            TEGECCATCATTECECTE 11523
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                                                                                                                                                                                                                                                                                                                                                                                                              MYCOBACTERIUM LEPRAE
E ADDRESS:
CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                    0;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                      2e+02;
                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                        Length 36412;
                                                                                                                                                                                                                                                                                                                    Indels
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US-08-968-505-15
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.8%; Score 14.4; Best Local Similarity 93.8%; Pred. No. 1 Matches 15; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15,
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                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Beck, James J.

TITLE OF INVENTION: Detection of Maize Fungal Pathogens
TITLE OF INVENTION: Using the Polymerase Chain Reaction
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                 STREET: 520
CITY: Tarrytown
CTATE: NY
                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer JB586"
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                                                                         ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           ZIP: 10591
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                                                                                                                                                                                                                                                                                                                                                USA
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(919) 541-8587
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38 GGCCATCAGTGCCCTG 53

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                                                                 Query Match
Best Local Similarity
                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                        TELEFAX: (650) 845-4166
NFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 264 base pairs
                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: UTRSNOT02
CLONE: 2260261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "primer JB586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                   RIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 93.8 les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UNFILING DATE: HEREWITH
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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GGCCATCAGTGCTCTG 19
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                                                       Conservative
                                                                                                                                                                                            linear
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                                                                                                                                                                                                            single
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93.8%;
                                                                    75.8%;
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Pred. No. 1.2e+02
                                                                     Score 14.4;
Pred. No. 1.
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                                                                     .6e+02
                                                                                     4; Length 264;
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                                                      Indels
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APPLICANT: Drmanac, Radoje T.

TITLE OF INVENTION: No. 6569662el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784C1P2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR APPLICATION NUMBER: 09/488,725

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Algate, Paul A.

FITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

FUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 327

LENGTH: 321

TYPE: DNA

ORGANISM: Homo sapiens

US-09-404-879A-327
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                                                       SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 769
LENGTH: 1071
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 646854
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APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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FEATURE:
NAME/KEY: CDS
LOCATION: (120)..(890)
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Local Similarity 93.8%;
les 15; Conservative
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                          Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Zhang, Jie
Ren, Feiyan
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Zhao, Qing A.
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Pred. No. 1.7e+02
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Sequence 6823, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev. TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 6823

LENGTH: 20

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-6823
                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/461,697; CURRENT FILING DATE: 1999-12-14; NUMBER OF SEQ ID NOS: 466; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 114; LENGTH: 132; TYPE: DNA; ORGANISM: Homo sapiens
US-09-461-697-114
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Best Local Similarity
Marches 16; Conserva
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US-09-198-452A-6823
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Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE,
APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-09-461-697-114/c
Sequence 114, Application US/09461697
Patent No. 6277974
                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                        APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
                                                                                       Local
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                                                                     l Similarity
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 CTGAGTCATCAGGGCTCTG
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93.8%;
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84.2%;
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Pred. No. 1.
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 22
                                                                    Score 14.2; DB 3;
Pred. No. 1.9e+02;
0; Mismatches 3
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                                                                                                        DB 3; Length 132;
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8
                                                                                                                                                             ; TYPE: DNA; ORGANISM: Homo sapiens US-09-461-697-112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
US-09-461-697-112/c
                                                                                                                                                                                                                                     APPLICANT: Lo, Donald C.
APPLICANT: Barney, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Portbury, Stuart D.
APPLICANT: Natz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CAMPOSITION SAND METHODS FOR DIAGNOSING
TITLE OF INVENTION: CELL DEATH
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                              Query Match
Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: COGENT NEUROSCIENCE, Inc
                                                                                                                                                                                                                         LENGTH: 141
49 CTGAGTCATCAGGGCTCTG
                                                                               16;
                                       1 CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627797
                                                                               Similarity 84.2
16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09461697
                                                                                                  74.7%;
84.2%;
                                                                                 0
                                                                                                     Score 14.2;
Pred. No. 1
                                                                                 Mismatches
                                                                                                     ; DB 3;
L.9e+02;
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Search completed: January 13, 2004, 17:58:45 Job time : 47.5 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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N_Geneseq_19Jun03:*

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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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21: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

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Gapop 10.0 , Gapext 1.0
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19
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and is derived by analysis of the total score distribution.	in or equ	Pred. No. is the number of results predicted by chance to have a
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f the	to the	esults
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SUMMARIES

c 8 19	c 7 19	c 6 19	c 5 19	c 4 19	c 3 15	2 1:	1 19	Result No. Score
9 100.0	9 100.0				9 100.0	9 100.0		,
1071	1068	1068	1068	1068	1068	19		Query Match Length DB
18	24	24	23	21	21	25	21	Ba
AAT79096	AAD25222	ABA94340	ABI97977	AAA35144	AAF21266	ABX12695	AAZ57602	ID
Human CCKR3 chemok	Human chemokine (C	Human CC chemokine	Non-endogenous hum	Human adenosine re	Human low adenosin	Human CCR3 recepto	Antisense oligonuc	Description

Antisense oligonucleotides directed to CCR3, interleukin or granulocyte

WPI; 2000-097743/08.

ALIGNMENTS

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RESULT 1
AAZ57602
ID AAZ5
XX
AC AAZ5
XX
DT 28-M
XX
DE Anti
XX
Anti
KW Anti
KW Anti
KW infl
XX
PD 23-I
XX
PF 17--
XX
PR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ57602 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9966037-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense oligonucleotide; CCR3 receptor; chemokine receptor; asthma; allergy; cancer; receptor expression inhibitor; hypereosinophilia; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-MAR-2000 (first entry)
                                                                                                                                                                                                    Renzi P;
                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense oligonucleotide CCR3AS to inhibit CCR3 receptor expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ57602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                (REEX-) RECH
                                                                                                                                                                                                                                                                                                EXPERTISES & DEV MEDICAUX PARENZ IN
                                                                                                                                                                                                                                                                                                                                                                                                98CA-2235420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-CA00572
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RESULT 2
ABX12695
ID ABX1
XX ABX1
AC ABX1
XX ABX1
XX Huma
XX Hope
XX Acyst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hypereosinophilia; cardiant; ophthalmological; cytostatic; antiasthmatic; antiallergic; antiinflammatory; immunosuppressive; atopic disease; neoplastic cell proliferation; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is an antisense oligonucleotide directed against the CCR3 receptor. The antisense oligonucleotide inhibits CCR3 receptor expression. The CCR3 receptor is important in the recruitment of eosinophils into the sites of allergic or asthmatic inflammation. The chemokines Botaxin, MCP-4 and RANTES mediate most of their effects through the CCR3 receptor. The invention relates to antisense oligonucleotides directed against a nucleic acid sequence encoding either a CCR3 receptor, a common subunit of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common subunit of IL-3, IL-5 and GM-CSF receptors. The antisense oligonucleotides can be used in the treatment or prevention of asthma,
                                  Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals involves incorporating into the nucleic acid molecule at least nucleotide substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       macrophage colony stimulating factor receptors, used for treating or preventing asthma, allergies, hypereosinophilia, inflammation or cancer
                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-2001; 2001US-303071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX12695 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 2 A; 6 C; 6 G; 5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-2002; 2002WO-CA01046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003004511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABX12695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergy, hypereosinophilia, general inflammation or cancer.
                                                                                                                                                                                                                                                                  ָם,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCR3 receptor DNA, antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Page 32; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation; 2'6'-diaminopurine; DAP; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19;
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                                                                                                                                                                                                                                                                                                                               TOPIGEN PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                               Allam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.
                                                                                                                                                                                                                                                                  Allakhverdi
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100.0%; Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #2
                                                                                               in mammals,
                                                                  least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
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AAF21266/c
ID AAF21266 standard; DNA; 1068 BP
XX
AC AAF21266;
XC AAF21266;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonu
XW Low adenosine antisense oligonu
XW human; airway disorder; broncho
XW immunosuppressive; antiasthmati
XW respiratory obstruction; pulmon
XW surfactant hypoproduction; pulmon
XW respiratory distress syndrome;
XW respiratory distress syndrome;
XW respiratory distress syndrome;
XW chronic obstructive pulmonary d
XW cancer; ss.
XX
DD 26-OCT-2000.
XX
PD 26-OCT-2000; 2000WO-US08020.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide cological molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cutaneous diseases, ophthalmological diseases, digestive diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, cancers. The respiratory system diseases is a sickness associated with can inflammation of the lungs, the airways and/or the nose. The respiratory system disease is a sickness associated with can inflammation of the lungs, the airways and/or the nose. The capiratory distress syndrome, cystic fibrosis, chronic obstructive clung disease, chronic bronchitis, eosinophilic bronchitis, asthma, can allergy, allergic rhinitis, sinusitis and hypereosinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. Cadenosine. ABX12681-ABX12698 represent antisense oligonucleotides of contenting at the case of the content of the case of the case of the content of the case of the case
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating or preventing atopic diseases proliferation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             low adenosine antisense oligonucleotide related sequence #2833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      obstructive pulmonary ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGGCCATCAGTGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neoplastic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
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RESULT 4
AAA35144/c
ID AAA351
XX
AC AAA351
XX
AC AAA351
XX
AC AAA351
XX
Human;
XX
Human;
KW Phosph
KW Phosph
KW allerg
KW antial
KW lung d
KW respir
KW pulmon
KW respir
KW pulmon
KW pulmon
KW respir
KW pulmon
KW Cancer
XX
PN WO2000
XX
PN WO2000
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobuling and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines receptors, adhesion molecules and their receptors, cytokine and chemokine receptors, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system central receptors, binding proteins and malignancy associated proteins. The care contistense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, condition selected from pulmonary vasoconstriction, inflammation, pulmonary transplantation respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, candor and antisons of chronic obstructive pulmonary disease (COPD), and or cancer. AAF18434 to AAF21543 represent human polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors,
                                                                                                                                                                                                                        Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
                                                                                                                                                                                                                                                                                                                                                                                Human adenosine receptor related polynucleotide 2nd SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA35144 standard; DNA; 1068 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1068 BP; 231 A; 289 C; 243 G; 305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 1182; 1592pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers and
                                                     WO200009525-A2
                                                                                                                                                                           respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; C
                                                                                                                                                        cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ragments and antisense oligonucleotides used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adenosine (A) content antisense oligonucleotides which gger adenosine receptors during metabolism, useful e.g. cers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGGGCCATCAGIGCICIG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                      lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19; DB 21; Length 1068; Pred. No. 5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                     NO:18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                do not
for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
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RESULT 5
ABI97977/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a new composition comprising an CC antisense oligonucleotide (ON) with low adenosine (up to 15%), which carries nucleic acids involved in bronchoconstriction, allergies, and/or CC inflammation. The ON can have antiinflammatory, antiallergic, cytostatic and analgesic activities. The compositions are CC useful for the treatment of diseases associated with inflammation, CC impaired airways, including lung disease and diseases whose secondary CC effects afflict the lungs of a subject. They can be used for treating CC esthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, CC carcinomas, and cancers which may metastasise to the lungs, including the relates of deoxyadenosine which may metastasise to the lungs, including CC carcinomas, and cancers. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the CC invention which correspond to SEQ ID NO:1 to 2815, and then the present cinvention, which correspond to SEQ ID NO:1 to 2815, and then the last CC (AAA32323 to AAA33992) are specifically claimed ONs from the present convention. N.B. Sequences given in the disclosure of the present CC invention do not match up with their corresponding SEQ ID NO: sequences given in the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                 Human; G protein-coupled receptor; GPCR; non-endogenous; mutant; constitutively activated GPCR; agonist; disease; ss.
                                                                                                                                                 Non-endogenous human GPCR cDNA, SEQ ID NO: 474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1068 BP; 231 A; 289 C; 243 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 1102; 1343pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchitis, emphysema, respiratory distress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension,
                                                               Homo sapiens
                                                                                                                                                                                     18-FEB-2002
                                                                                                                                                                                                                    ABI97977;
                                                                                                                                                                                                                                                      977/c
ABI97977 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-) UNIV
                                                                                                                                                                                                                                                                                                                                         105
                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                            CTGGGCCATCAGTGCTCTG
                                                                                                                                                                                                                                                                                                                                         CTGGGCCATCAGTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAST CAROLINA
                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                        CDNA; 1068
                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 19;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                          19
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          5.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1068;
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WO200177172-A2

Synthetic

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RESULT 6
ABA94340/c
ID ABA943.
XX
AC ABA943.
XX
AC ABA943.
XX
DT 26-MAR
XX
DT 26-MAR
XX
CC che
KW CC che
KW antias
KW antipr
XX
FT CDS

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Best Local S
Matches 19
      WPI; 2002-114347/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to G protein-coupled receptors (GPCRs) for which the endogenous ligand has been identified. Non-endogenous constitutively activated versions of known GPCRs are used in the invention for the direct identification of candidate compounds as receptor agonists, inverse agonists or partial agonists. Such agonists are useful as therapeutic agents for diseases or disorders associated with GPCRs. The present sequence encodes a non-endogenous version of a known human GPCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying agonists of G protein-coupled receptors (GPCRs) disease treatment, comprises contacting candidate compounds versions of GPCRs -
                                                    Barnes AA,
                                                                                                                                                                                                            31-MAY-2001; 2001WO-EP06195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC chemokine receptor-3; CCR3; antiallergic; antiinflammatory; human; antiasthmatic; ophthalmological; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CC chemokine receptor 3 (CCR3) encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antipruritic;
                                                                                                                                                          01-JUN-2000; 2000GB-0013345
                                                                                                                                                                                                                                                                06-DEC-2001
                                                                                                                                                                                                                                                                                                                  WO200192520-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA94340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABA94340 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1068 BP; 232 A; 288 C; 244 G; 304 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehmann-Bruinsma K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-APR-2000; 2000US-195747P
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                                                                                                          (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AREN-) ARENA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-648759/74.
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            creeccarcaerecrere
                                                    Fraser NJ, O'Shaughnessy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds.
                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    /product= "CCR3"
                                                                                                                                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 19; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liaw
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                                                      ÇŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.9;
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                                                        Wise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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AAD25222/c
ID AAD25222 standard; cDNA; 1068 BP
XX
AC AAD25222;
XX
DT 12-MAR-2002 (first entry)
XX
C Human chemokine (C-C motif) rece
XX
Human; chemokine (C-C motif) rece
XX
Human immunodeficiency virus 1;
XX
Chromosome 3p21.3; ss.
XX
OS Homo sapiens.
XX
YX
Chromosome 3p21.3; ss.
XX
OS Homo sapiens.
XX
PT variation replace (51, C)
FT variation /*tag= a /*standard name=
FT variation replace (1052, C)
FT rectance replace (1052, C)
FT replace (1052, C)
FT rectance replace (1052, C)
FT replace (1052, C)
FT rectance replace (1052, C)
FT rep
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stabilize or enhance expression of the receptor in a cell membrane. Assays for investigating properties of the CCR3 receptor are useful for the identification of modulators of eotaxin-mediated CCR3 receptor activity. The identified modulators are useful in the treatment of prophylaxis of allergic or inflammatory disorders which are responsive to regulation of CCR3 receptor activity. The agents are also useful in the treatment of allergy or asthma as well as ophthalmological, inflammatory, gastrointestinal, dermatological, respiratory or pruritic disorders. The agents are useful for treating conjectivitis, inflammatory bowel disease, eczema, allergic rhinitis, nasal polyposis, atopic dermatitis and pruritis, chronic obstructive pulmonary disease (COPD) and other lung disorders and immune disease. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping; genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy; human immunodeficiency virus 1; single nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified CC chemokine receptor-3 useful for identifying modulators of eotaxin-mediated CCR3 receptor for treating allergic and inflammatory disorders, comprises modifications to stabilize or enhance surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human chemokine (C-C motif) receptor 3 (CCR3) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1068 BP; 231 A; 289 C; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 25-26; 29pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABB07240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCR3 receptor encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a CC chemokine receptor-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGCCATCAGTGCTCTG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises
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                                                                                                                                                                                                                                                                                                                                                                    /product= "Human replace (1052, C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers replace (51, C)
                                                                                                                                                                                                                                                                           /standard_name= "Single nucleotide polymorphism (SNP)"
/note= "Polymorphic site (PS) 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard name= "Single nucleotide
/note= "Polymorphic site (PS) 3" ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 CCR3
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                                                                                                                                                                                                                                                                                                                                                                                               protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24;
5.9;
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XX CCF18
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The present sequence is human CCR3 CDNA. The CCR3 gene is located on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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    Dairaghi DJ,
                                                                                                                    08-DEC-1995;
                                                                                                                                                                          05-DEC-1996;
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                                                        (SCHE ) SCHERING CORP
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)B; AAE15320.
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                emokine; mouse; primer; PCR; amplification; antagonist; hum.
physiology; development; anti-viral; probe; hybridisation;
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  Hara T,
                                                                                                                    95US-0567882
                                                                                                                                                                          96WO-US19139
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                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= CCKR3 chemokine receptor
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  Miyajima A,
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       Schall TJ,
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Best Local S
Matches 19
A consensus DNA sequence (AAT31336) codes for a novel human recept (AAW03378), designated Eos L2 or C-C chemokine receptor 2 (CKR-3). It was deduced by comparing a genomic clone (AAT31334) and a cDNA clone (AAT31335) coding for CKR-3 proteins (AAW03376 and AAW03377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the nucleotide sequence encoding a novel CCKR3 chemokine receptor isolated from a Th0-activated human T-cell cDNA library using the sequence amplified by primers AAT79097 and AAT79098 as a probe. The encoded protein can be used to screen for (ant) agonists that bind to the novel CCF18 chemokines (AAW25941 and AAW25942). These (ant) agonists are useful in the treatment of conditions associated with abnormal physiology or development.
                                                                                                                                                                    Mammalian chemokine receptor-3 and related nucleic identify receptor inhibitors to treat inflammatory autoimmune disorders, certain cancers, etc.
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                                                                                                                                                                                                                                                                       WPI; 1996-354528/35.
P-PSDB; AAW03378.
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P-PSDB; AAW25943.
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                                                                                                                       153pp; English.
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disease, e.g.
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Best Local S
Matches 19
novel human C-C chemokine receptor 3, also designated CKR-3, CCR3 or Eos L2, that binds and mediates chemotaxis in response to chemokines such as eotaxin, RANTES and MCP-3. Sequence comparison revealed 2 regions in the cDNA sequence that appeared to be shifted in frame, resulting from an insertion of a base followed by the deletion of a base, or the deletion of a base followed by the insertion of a base. These alterations resulted in 4 contiguous amino acid differences in the predicted proteins (see AAW51744 and AAW51745) at positions 263-266 and 276-279, respectively. In addition, the genomic clone codes for threonine (ACG) at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7404/c
AAV07404
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                                                                                                                                                                                                                                                                                                                                                                                              Antibodies to chemokine receptor-3 protein - useful and treatment of inflammatory conditions, e.g. aller autoimmune disease, graft rejection or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human; G protein-coupled receptor; leukocyte; antibody; antagonist; inflammation; allergy; asthma; graft rejection; infection; autoimmune disease; drug screening; therapy; ds.
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                                                                                                                                                                                                                                                                     This is a consensus sequence constructed by alignment of a genomic DNA sequence (see AAV07402) and a cDNA clone (see AAV07403) coding
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 137-138; 185pp; English.
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Qin S;
 A genomic DNA clone (AAT31335) codes for a novel receptor (AAW03 designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved in leukocyte migration associated with inflammation. It was isolated from a human library constructed from eosinophils obtd. from a patient with hyper-eosinophilic syndrome using a probe (p4 cDNA) encoding the MIP-lalpha/RANTES receptor. A CKR-3
                                                                                                                                                                                                      Mammalian chemokine receptor-3 and related nucleic acids - useful identify receptor inhibitors to treat inflammatory disease, e.g. autoimmune disorders, certain cancers, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              position 276 and the cDNA clone for serine (AGC). The predicted amino acid sequence from the consensus is given in AAW51747. CKR-3 nucleic acids, polypeptides, antibodies, agonists and antagonists are useful for diagnosis and treatment of
                                                                                                                                                           Claim 1; Page 111-113; 153pp; English.
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DB; AAW03377.
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LEUKOSITE INC.
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tory; eosinophil; ss.
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918..919
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This cDNA codes for novel human C-C chemokine receptor 3 (see C AAW51745), also designated CKR-3, CCR3 or Eos L2, that binds and mediates chemotaxis in response to chemokines such as eotaxin, C RANTES and MCP-3. The cDNA was isolated from a human eosinophil C cDNA library constructed from eosinophils obtained from a patient C with hypereosinophilic syndrome, and using CKR-1 cDNA as probe. A C genomic DNA sequence (see AAV07402) is also provided as well as a C consensus sequence (see AAV07404) for CKR-3. The invention relates C to isolated and/or recombinant nucleic acids encoding CKR-3, C isolated or recombinant CKR-3 polypeptides, recombinant nucleic acid constructs, host cells useful for production of recombinant C CKR-3 proteins, to antibodies reactive with the receptors, and to methods of using these products to identify ligands, antagonists and agonists of receptor function. Inhibitors of CKR-3 can be used to treat: inflammatory or allergic diseases and conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies to chemokine receptor-3 protein - useful for diagnosis and treatment of inflammatory conditions, e.g. allergy, asthma, autoimmune disease, graft rejection or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Page 134-136; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-C chemokine receptor 3; CKR-3; CCR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; leukocyte; antibody; antagonist; inflammation; allergy; asthma; graft rejection; infection; autoimmune disease; drug screening; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LEUK-) LEUKOSITE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-286418/25.
DB; AAW51745.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGCCATCAGTGCTCTG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemokine receptor 3 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ponath PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0720565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US17103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA; 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eos L2; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 1193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .9
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cresponses, drug allergy, insect sting allergy, inflammatory bowel
cdisease, such as Crohn's disease and ulcerative colitis,
cdermatosis such as dermatitis, eczema, atopic dermatitis,
cdermatosis such as dermatitis, urticaria, vasculitis (e.g. necrotizing,
cutaneous and hypersensitivity vasculitis); eosinphilic myositis
cand eosinophilic fasciitis; autoimmune diseases such as rheumatoid
carthritis, psoriatic arthritis, multiple sclerosis, systemic lupus
crythematosus, myasthenia gravis, juvenile onset diabetes,
cardinary including allograft rejection or graft-versus-host
cdisease; cancers with leukocyte infiltration of the skin or organs;
and also reperfusion injury, atherosclerosis, certain haematologic
malignancies, septic shock and endotoxic shock. Promoters of CKR-3
cfunction can be used for treating: immunosuppression e.g. in AIDS
cpatients or individuals undergoing radiation therapy, chemotherapy,
ctherapy for autoimmune disease or other drug therapy, and
conther causes; and infectious disease such as parasitic diseases,
cincluding helminth infections, such as nematodes (round worms).

Chemotograft can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                                                                 Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  including respiratory allergic diseases such as asthma, allergic rhinitis, hypersensitivity lung disease, hypersensitivity pneumonitis, eosinophilic pneumonia (e.g. Loeffler's syndrome, chronic eosinophilic pneumonia, interstitial lung disease (ILD) e.g. idiopathic pulmonary fibrosis or ILD associated with rheumatoid arthritis, systemic lupus erythematosus, ankylosing spondylitis, systemic sclerosis, Sjogren's syndrome, polymyositis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human low adenosine antisense oligonucleotide related sequence #2834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF21267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF21267
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1193 BP; 274 A; 310 C; 275 G; 334 T; 0 other;
                                                                                                                                                                WO200062736-A2
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                                                                                                                                                                                                                                                    88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCCATCAGTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA; 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 19; I
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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06-APR-1999;

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(UYEC-) UNIV EAST CAROLINA

24-MAR-2000; 2000WO-US08020

26-OCT-2000.

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AAA35145/c
ID AAA351
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DE Human
DE Human;
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KW allerg
KW antial
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OS Homo s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cc immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. Cc The antisense oligonucleotides and (I) can be used to down-regulate the cexpression and or activity of target polypeptides associated with clung/respiratory disorders and malignancies, such as stimulating and communoglobulins and antibodies, antibody receptors, cytokines and communoglobulins, adhesion molecules and their receptors, cytokine and commonkine receptors, adhesion molecules and non-nervous system peptides and receptors, defensins, growth factors; vasoactive peptides and committers, defensins, growth factors; vasoactive peptides and communities, binding proteins and malignancy associated proteins. The concluding respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) cand/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory diserses syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary cransplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polymucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; Condition; and cystic fibrosis; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oligonucleotides and compositions oligonucleotides the A is replaced (I) can have respiratory, bronchoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g. cancers and respiratory obstructions -
     Homo sapiens
                                                                   respiratory distress syndrome; pain; cystic fibrosis; emphysema pulmonary hypertension; chronic obstructive pulmonary disease;
                                                                                                                                                                                                                                                                                               28-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present
                                              cancer; leukaemia;
                                                                                                                                                                                                                                                 Human adenosine receptor related polynucleotide 2nd SEQ ID NO:19.
                                                                                                                                                                                                                                                                                                                                                                                   AAA35145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
                                                                                                                                                                                                       adenosine receptor; low adenosine antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGGCCATCAGTGCTCTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1201 BP; 278 A; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention describes low adenosine (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                               (first entry)
                                            lymphoma; carcinoma; metastasis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; s
100.0%; F
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ositions (I) comprising them. In the antic
replaced by a 'Universal' or alternative
bronchodilator, antiinflammatory, analges
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1201;
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                                                                     COPD;
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                                                                                                                                                                                                           RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                            impaired airways, including lung disease and diseases whose secondary conditions, including lung disease and diseases whose secondary conditions, impeded respiration, respiratory vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the crelease of deoxyadenosine which activates adenosine receptors causing conchoconstriction and inflammation. AAA32313 to AAA35312 represent the invention, which correspond to SEQ ID NO:1 to 2815, and then the last of Sequences are also called SEQ ID NO:1 to 185, but the sequences of invention. N.B. Sequences given in the disclosure of the present convention do not match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                                                                                                                                                                    Best
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, immaired airmonic including the composition of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyce JW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1201 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1102; 1343pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1999;
                                                                                                                                                                          ABK84282 standard; cDNA; 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200009525-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYEC-)
                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                   in the
                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                           CTGGGCCATCAGTGCTCTG 118
                                                                                                                                                                                                                                                                                        CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  sequence listing.
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                                                                                                                                                                                                                                                                                                                                                                                   278 A;
                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                      .0%; Score 19;
                                                                                                                                                                                                                                                                                                                                                                                    320 C; 267
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                                                                                                                                                                                                                                                                                                                                                                                      336 T; 0
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                                                                                                                                                                                                                                                                                                                                                       Length 1201;
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                                                                                                                                                                                                                                                                                                                         Gaps
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the

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Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis

14-AUG-2002

(first entry)

CDNA

differentially expressed in granulocytic cells #853

ABK84282;

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The invention relates to detecting (M1) granulocyte (GC) activation (CC (GCA), by detecting the level of expression of gene(s) (Ge) identified by CC (DNA (hip analysis as given in the specification, and comparing CC (he expression level to an expression level in an unactivated (GC), where differential expression of GB is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent (CC (has alters the expression of at least one gene in Gs; (2) screening (M3) (CC (chronic)) in a tissue, an allergic response in a subject, exposure of a (CC (subject to a pathogen or sterile inflammatory disease using the (CC (chronic)) in a tissue, an allergic response in a subject, exposure of a (CC (chronic)) in a tissue, an allergic response in a subject, exposure of a (CC (chronic)) in a tissue, an allergic response in a subject, exposure of a (CC (chronic)) in a tissue, an allergic response in a subject, exposure of a (CC (chronic)) in a tissue, an allergic response of gene(s) from GS, where (CC (chronic)) in a tissue, an allergic response of gene(s) from GS, where (CC (chronic)) in a tissue, an allergic response of sintlammation, (especially chronic) or in a tissue, where (CC (chronic)) in a tissue of the gene is indicative of inflammation, (especially chronic) or in a tissue, and lergic response in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue having (CC) inflammation with an agent that modulates the expression of gene(s) (CC) proferably in an inflammation in a tissue, M4 is useful for certaining an agent capable of modulating (CC) and the tissue, M2 is useful for condulating GA, M3 is useful for screening an agent capable of modulating (CC) appreciably in an inflammation in a tissue, M4 is useful for condulating GA, M3 is useful for screening an agent capable of modulating (CC) appreciably in an inflammation in a tissue, M4 is useful for condulating (CC) appreciably benefit of the profession of the profession of the profession of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
Sequence 1201 BP; 278 A; 320 C; 267 G; 336 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 853; 114pp; English
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                                                                                          ftp.wipo.int/pub/published_pct_sequences.
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    other;
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CTGGGCCATCAGTGCTCTG 19

Query Match Best Local

Similarity

100.0%;

Score 19; 1 Pred. No. 5 Mismatches

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Gaps

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DB 24; Length 1201;

Conservative

<u>o</u>

Matches

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RESULT 16
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ID ACA56
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                                                                                                                                                                                                                                                                                                          cc array element in a microarray for monitoring the expression of a number cd diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in the cd diagnosis and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, cforensics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose coding for different signaling cancer e.g. adenocarcinoma and leukaemia, communopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease coding and parkinson's disease. The present sequence represents a polynucleotide probe of the invention.

CC Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequalta.uspto.gov/sequence.html?DocID=06500938B1.
                                                                                                                             Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1487/c
ACA56487 standard; cDNA; 1201 BP
                                                                                                                                                                                                                                                          Sequence 1201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target
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                                                                                                                               Conservative
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                                                                                                                             Score 19; DB 2
Pred. No. 5.9;
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                                                                                                                                                                                                                                                             G; 336 T; 0 other;
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                                                                                                                                                                                          Length 1201;
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RESULT 17
ABZ42635/c
XX
ABZ42635/c
ABZ42636/c
ABZ4263/c
ABZ4260/c
ABACC ABACC
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(C) (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (I) an assay for the detection of a particular CC acids. Also described: (I) an assay for the detection of a particular CC and (2) an isolated antibody having high specificity and high affinity CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting CC antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the CC presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell cregeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AlDS, Alzheimer's diseases, cute carterial, fungal, protozoan or viral infections,
                                                                                 osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease cancer or autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human C-C chemokine receptor 3 nucleotide SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-2000; 2000US-257144P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Sequence 1201

BP; 278

A; 320

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267 G;

336 T;

0 other

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RESULT 18
AAT31334/c
ID AAT313
XX AAT31334/c
ID AAT313
XX IS AAT313
XX IS AAT313
XX AAT31334/c
ID AAT31334/c
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IS AAT3134
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Best Local Similarity
Matches 19; Conserv
                        A genomic DNA clone (T31334) codes for a novel receptor (W03376), designated Eos L2 or C-C chemokine receptor 3 (CKR-3), involved in leukocyte migration associated with inflammation. It was isolated from a human genomic library in EMBL3 SP7/T7 vector by screening with a PCR fragment generated from eosinophil cDNA using degenerate primers (see also T31337-44). A CKR-3 cDNA clone (T31335) was also isolated, and a consensus sequence is given in T31336. The genomic and cDNA clones can be used for the prodn. of recombinant CKR-3 in host cells, or to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerard
Qin S;
                                                                                                                                                                                                                                                                                                  Mammalian chemokine receptor-3 and related nucleic identify receptor inhibitors to treat inflammatory autoimmune disorders, certain cancers, etc.
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-354528/35.
P-PSDB; AAW03376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC-chemokine
                                                                                                                                                                                                                                                           Claim 1; Page 109; 153pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BGHM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC-chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT31334;
       antisense sequences useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9622371-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT31334 standard; DNA; 1689 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 CTGGGCCATCAGTGCTCTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRIGHAM & WOMENS HOSPITAL.
CHILDRENS MEDICAL CENT.
LEUKOSITE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor 3; CKP-3; Eos-L2; tory; eosinophil; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor 3 genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0375199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "CKR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1007..1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP,
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in the
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1007-1008, coding for threonine
position 276; a cDNA clone has C
these positions, coding for seri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mackay CR,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at position 1291 specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ponath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibitor; antisense,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U)
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5.9;
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                                                                                                                                                                                                                                                                                                                                disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TW;
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     myasthenia gravis; juvenile onset diabetes; glomerulonephritis; autoimmune; thyroiditis; Bechet's; graft; rejection; transplantation; allograft; graft versus host; cancer; leukocyte infiltration; reperfusion injury; atherosclerosis; haematologic malignancy; septic; endotoxic; shock; polymyositis; dermatomyositis; immunosuppression; immunodeficiency AIDS; radiation therapy; chemotherapy; autoimmune; corticosteroid; C-C chemokine receptor 3; CRK3; ss.
The present sequence encodes human C-C chemokine receptor 3 (CRK3), to which human eotaxin (hE), an eosinophil specific chemoattractant
                                                                                                                                                                                                                                                                                                             WO9700960-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatoid arthritis; systemic; lupus erythematosus; SIE; ankylosing spondylitis; sclerosis; Sjorgen's; polymyositis; dermatomyositis; bowel; anaphylaxis; drug; penicillin; cephalosporin; insect sting; Crohn's; ulcerative colitis; spondyloarthropathy; scleroderma; psoriasis; dermatosis; dermatitis; eczema; atopic; urticaria; necrotising; cutaneous; vasculitis; myositis; fascitis; multiple sclerosis;
                                        Example 7; Page 97; 130pp; English
                                                                    New isolated human eotaxin gene - used to develop prods. for the diagnosis and treatment of e.g. inflammation, allergies, auto-imdisease, infections and tumours
                                                                                                                                                                   MacKay C,
                                                                                                                                                                                                                                                                                   09-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  accumulation; attraction; chemotaxis; diagnosis; prevention; treatment; disease; inflammation; allergy; asthma; rhinitis; hypersensitivity; lung; pneumonia; Loeffler's; syndrome; interstitial; LD; idiopathic pulmonary fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human C-C chemokine receptor 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1689 BP; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1997 (first entry)
                                                                                                                                                                                                                           23-JUN-1995;
                                                                                                                                                                                                                                                       21-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT58783
                                                                                                                                                                                                (LEUK-) LEUKOSITE INC.
                                                                                                                            1997-087387/08.
DB; AAW10100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA; 1689
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                                                                                                                                                                   Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                            95US-0494093.
                                                                                                                                                                                                                                                       96WO-US10723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eosinophil; chemoattractant; stimulation;
                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
181..1248
                                                                                                                                                                                                                                                                                                                                       /product= CRK3
                                                                                                                                                                                                                                                                                                                                                     /*tag=
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                                                                                                                                                                      Ponath
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; 344 G; 497 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA.
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                                                                                                                                                                  Ringler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodeficiency;
                                                                                   auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
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AC AAVC
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DE Huma
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C-C
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KW infl
KW autc
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OS Homc
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FH Key
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                                                                                                                                                                                                                                                                                                                                                               RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC rhintitis, hypersensitivity lung diseases (e.g. decimoshilic pneumonias such as Loeffler's syndrome and chronic CC eosinophilic pneumonia, interstitial lung diseases (ILD) such as CC didopathic pulmonary fibrosis or ILD associated with rheumatoid CC arthritis, systemic sclerosis or ILD associated with rheumatoid CC spondylitis, systemic sclerosis, Sjorgen's syndrome, polymyositis or dermatomyositis), systemic anaphylaxis or hypersensitivity CC responses, drug allergies (e.g. to penicillin and cephalosporins), CC insect sting allergies, inflammatory bowel diseases (e.g. Crohn's CC disease and ulcerative colitis), spondyloarthropathies, cc urticaria and necrotising, cutaneous and hypersensitivity careful tis, eosinophilic myositis and fascitis, multiple contact dermatitis, eosinophilic myositis and fascitis, multiple coloresis, SLE, myasthenia gravis, juvenile onset disease, graft crigomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft crigomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft CC glomerulonephritis, autoimmune thyroiditis, Bechet's disease, graft crigomerulonephritis, autoimmune thyroiditis, bechet's disease, graft crigomerulonephritis, autoimmune thyroiditis, contact cheration or graft versus host disease and cancers with leukocyte infiltration or fifthe skin or organs. The products can also be used to treat other cdiseases or conditions requiring the inhibition of undesirable crigomerulonephritis, immunosuppression (e.g. in individuals with immunosuppression (e.g. in individuals with immunosuppression), cherapy, cherapy, cherapy, which causes or other drug therapy, such as corticosteroid therapy, which causes condential) cd diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                             C-C chemokine receptor 3; CKR-3; CCR3; Eos L2; human; G protein-coupled receptor; leukocyte; antibody; antagonist; inflammation; allergy; asthma; graft rejection; infection; autoimmune disease; drug screening; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Degenerate primers based on the guinea pig eotaxin amino acid sequence were used for the reverse transcriptase polymerase chain reaction (RT-PCR) amplification of RNA isolated from inflamed, eosinophilic lung tissue obtained from Balb/c mice sensitised to ovalbumin. The amplification product was used as a probe to screen a human genomic library in vector EMBL3 SP6/T7 to obtain the hE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eosinophils (including chemotaxis), binds.

hE can be used to develop products for the diagnosis, preventic treatment of hE associated diseases or conditions. The products be used to treat inflammatory or allergic diseases and conditions including respiratory allergic diseases (e.g. asthma, allergic diseases).
                                                                                                                                                                                         Human C-C
                                                                                                                                                                                                                                  28-SEP-1998
                                                                                                                                                                                                                                                                              AAV07402;
                                                                                                                                                                                                                                                                                                                     402/c
AAV07402 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1689 BP; 431 A; 416 C; 344 G;
                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     capable of stimulating eosinophil accumulation and/or attracting
                                       варіепв
                                                                                                                                                                                                                                                                                                                                                                                                                               285
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGGGCCATCAGTGCTCTG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                       chemokine receptor 3 genomic DNA.
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                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                         1689
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Location/Qualifiers

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30-SEP-1996;
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                                                                                                                                                                  Example 2; Fig 1A-C; 185pp; English.
                                                                                                                                                                                               Mackay CR, Ponath PD
                                                                                                                                                                                                      (LEUK-) LEUKOSITE INC
                                                                                                                                                        genomic DNI
AAW51744),
                                                                                                                                                                                         1998-286418/25.
                                                                                                                                                                        disease, graft rejection or cancer
     can also be used for
                                                                                                                                                            DNA codes for novel human C-C
                                                                                                                                                                                                            96US-0720565.
                                                                                                                                                                                                                   97WO-US17103.
                                                                                                                                                                                                                                         181..1248
      detection
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CC RANTES and MCP-3. The DNA was isolated from a human genomic phage CC library using as probe a PCR fragment that had been generated from CC chemokine receptor genes. A cDNA clone (see ANV07405-12) based on known CC chemokine receptor genes. A cDNA clone (see ANV07403) for CKR-3 is CC also provided. Comparison of the sequences suggests that the CC genomic DNA has an intron that separates the promoter and most CC of the 5' untranslated region from the coding region. A consensus CC of the 5' untranslated region from the coding region. A consensus CC of the French and cDNA sequences is provided (see ANV07404). The CC invention relates to isolated and/or recombinant nucleic acids constructs, host cells useful for production of recombinant CKR-3 proteins, to antibodies reactive CC dientify ligands, antagonists and agonists of receptory or allergic clientify ligands, antagonists and agonists of receptor function. CC Inhibitors of CKR-3 can be used to treat: inflammatory or allergic clientify ligands, antagonists and agonists of receptor function. CC indentify ligands, antagonists and agonists of receptor function. CC indentify ligands, antagonists and agonists of receptor function. CC indentify ligands, antagonists, including respiratory allergic diseases compared the products to associated with rheumatoid ecsinophilic pneumonia (e.g. C. Loeffler's syndrome, chronic cosinophilic pneumonia, interstitial CC ankylositis or dermatcomyositis), systemic supulporary fibrosis or ILD cassociated with rheumatoid arthritis, systemic supulporary syndrome, CC inflammatory bowel disease, such as Crohm's disease and ulcerative CC inflammatory bowel disease, such as Crohm's disease and ulcerative CC inflammatory bowel disease, such as Crohm's disease and ulcerative CC inflammatory bowel disease, such as crohm's disease such as rheumatoid carchitis, such as dermatitis, unclaitis escentisis, systemic lupus content carchitis, autoimmune diseases such as rheumatoid carchitis, autoimmune diseases such as rheumatoid carchitis, autoimmune
                                                                                                                                                     erythematosus, myasthenia gravis, juvenile onset diabetes, glomerulonephritis, autoimmune thyroiditis and Behcet's disease; graft rejection, including allograft rejection or graft-versus-host disease; cancers with leukocyte infiltration of the skin or organs; and also reperfusion injury, atherosclerosis, certain haematologic malignancies, septic shock and endotoxic shock. Promoters of CKR-3 function can be used for treating: immunosuppression e.g. in AIDS patients or individuals undergoing radiation therapy, chemotherapy, therapy for autoimmune disease or other drug therapy, and immunosuppression due congenital deficiency in receptor function or other causes; and infectious diseases such as parasitic diseases, including helminth infections, such as nematodes (round worms).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies to chemokine receptor-3 protein - useful for diagnosis and treatment of inflammatory conditions, e.g. allergy, asthma,
Sequence 1689
BP; 431 A; 416 C; 344
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    <u>ရ</u>
    497 T; 1 other
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XX Inw MPI; 2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                 The present invention describes low adenosine (A) content antisense CC oligonuclectides and compositions (I) comprising them. In the antisense CC oligonuclectides the A is replaced by a 'Universal' or alternative base. CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. CC The antisense oligonuclectides and (I) can be used to down-regulate the CC carpession and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and CC activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and CC chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and contral receptors, defensins, growth factors, vasoactive peptides and contral receptors.
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Matches 19
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transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 1183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-679539/66.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF21268;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYEC-) UNIV EAST CAROLINA (NYCE/) NYCE J W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                           The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-205971/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy;
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Pred. No.
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RESULT 23
ABL40462/c
ID ABL404
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AC ABL404
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AC ABL404
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DT 10-JUN
XX
DE Human
XX
Mucosa
KW CCR3;
KW CCR3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 19
                                                                                                        Identifying modulators of mucosae-associated epithelial chemokine (MEC) receptors 3 or 10 (CCR3/10), useful for treating inflammatory diseases, comprises detecting formation of MEC-CCR3/10 complex or modulation of a MEC-induced response -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mucosae-associated epithelial chemokine; MEC; CCR3; CCR10; anti-inflammatory; cytostatic; ir antibacterial; chemokine; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL40462 standard;
                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human C-C chemokine receptor 3 (CCR3) protein encoding cDNA
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DB; ABB07733.
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UNIV LELAND STANFORD
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c: C-C chemokine receptor;
immunomodulator; anti-viral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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The invention relates to identifying agents that inhibit or promote the

Example 2;

Fig 4A-B; 92pp; English.

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RESULT 24
ABX13645/c
ID ABX136
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AC ABX136
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; ss; gene; mucosae-associated epithelial chemokine; MEC; chromosome 5; C-C chemokine receptor; CCR3; CCR10; allergy; IgA antibody-secreting cell; inflammatory disease; Sjogren's syndrome; oral inflammatory condition; Behcet's syndrome; mastitis; chronic obstructive lung disease; asthma; inflammatory bowel disease; IgA nephropathy; dermatitis herpetiformis; ulcerative colitis; coeliac disease; autoimmune disease; arthritis; multiple sclerosis; systemic lupus erythematosus; myasthenia gravis; diabetes; autoimmune thyroiditis; graft rejection; atherosclerosis; cancer; infectious disease; immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding of a mammalian
                                        WPI; 2003-102382/09.
P-PSDB; ABG72634.
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                                                                                                                                                Butcher EC,
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181..1248
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                                                                                                                                                                                                                        PHARM INC
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The invention relates to identifying an agent which inhibits or promotes the binding of mammalian MEC (mucosae-associated epithelial chemokine) to CC a mammalian C-C chemokine receptor 3 (CCR3) or CCR10 comprising a CC (a) combining an agent to be tested, a composition comprising a CC naturally occurring mammalian (CCR3). CCR10 or MEC-binding variant, and a CC mammalian MEC; and (b) detecting or measuring the formation of a complex between the MEC and the CCR3, CCR10 or MEC-binding variant. The CC method alternatively comprises: (a) combining an agent to be tested, a CC cell expressing a protein comprising a maturally occurring mammalian (CCR3, CCR10 or MEC-binding variant, and a mammalian MEC under conditions (CCR3, CCR10 or MEC-binding variant, and a mammalian MEC under conditions (CCR3, CCR10 or MEC-binding variant, and a mammalian MEC under conditions (CCR3, CCR10 or MEC-binding the agent indicates that the agent is an inhibitor or promoter. Also included are: (1) an immunoglobulin or antigen-binding fragment which binds a naturally occurring mammalian CCR3 or CCR10, and inhibits the binding of a contitity of an IgA antibody-secreting cell in a subject, comprising (CCMEC occurring mammalian MEC to the receptor; and (2) modulating the CCR3 and/or CCR10. The methods and compositions of the present condition such as oral inflammatory condition (e.g., Sjogren's or CCR Behcet's syndrome), mastitis, chronic obstructive lung disease or altergic condition such as oral inflammatory condition (e.g., Sjogren's or CCR Behcet's syndrome), mastitis, chronic obstructive lung disease, asthma, CC uncerative colitis and coeliac disease. They can also be used in CC autoimmune diseases such as arthritis, multiple sclerosis, cancers, infectious (diseases and disorders are CC diseases and disorders are CCR3. The present sequence is the Human cDNA encoding C-C chemokine CCR3. The present sequence is the Human cDNA encoding C-C chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying agents that inhibit or promote binding of mammalian MEC CCR3 or CCR10, useful for treating an inflammatory and autoimmune diseases, atherosclerosis, cancers, infectious diseases, diabetes, arthritis and asthma -
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               S
                                 Matches
                                          Best
                                                 Query Match
                                         Local
285
                                 l Similarity
19; Conserv
          1 CTGGGCCATCAGTGCTCTG 19
CTGGGCCATCAGTGCTCTG 267
                                 Conservative
                                         100.0%;
                                                100.0%;
                                 0,
                                          Score 19;
Pred. No.
                                  Mismatches
                                         6.2;
                                                 DB 25; Length 1689;
                                 0;
                                  Indels
                                 0
                                 Gaps
                                 0,
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Sequence 1689 BP; 430 A; 416 C; 345 G; 497 T; 1 other;

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ABL67066/c
ID ABL670
XX
AC ABL670
XX
DT 15-MAY
XX
DE Thyroi
XX
Cytost
KW Human;
KW Stomac
KW Gytost
KW Gene;
XX
DS Homo 8
XX
PN WO2001
XX
PD 13-DEC
XX
PF 30-MAY
                                                                                                                                                                                                                                                                                                                                        RESULT 25
                                                                                                                                             Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                          15-MAY-2002
                                                                                                                                          cytostatic; gene therapy; antineoplastic;
                                                                                                                                                                                                           Thyroid cancer related gene
                                                                                                                                                                                                                                                                                                          ABL67066 standard; DNA; 1717
                                                               WO200194629-A2
                                                                                                                                                                                                                                                                           ABL67066;
                                                                                             Homo sapiens.
                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                           sequence SEQ ID NO:5403.
                                                                                                                                                                                                                                                                                                          ВP
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30-MAY-2001; 2001WO-US10838.

13-DEC-2001

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The present invention describes a method (M1) for screening for an CC anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in CC expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in CC expression is indicative of anti-neoplastic activity. (I) has cytostatic expression is indicative of anti-neoplastic activity. (I) has cytostatic cativity and can be used in gene therapy. M1 can be used for screening anti-neoplastic agent, and can be used for product which compared to the data collected with respect to the anti-neoplastic agent as a coll structure and/or properties of the agent. M1 can be used in the creatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinema, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, squamous cell carcinoma, neuroendocrine
                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2000;
20-SEP-2000;
22-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
27-SEP-2000;
28-SEP-2000;
28-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
                                                                                                                                                                                                                                                                                                                       Young P
                                                                                                                                                                                                                                          Screening for anti-neoplastic agent involves exposing cells chemical agent to be tested for anti-neoplastic activity, an determining a change in expression of a gene of a signature
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                                                                                                                                                                                                                     Claim
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DR,
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                                                                                                                                                                                                                     SEQ
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Weaver Z
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2000US-236119P.
2000US-236111P.
2000US-236842P.
2000US-237172P.
2000US-237173P.
2000US-237278P.
2000US-237278P.
2000US-237294P.
2000US-237316P.
2000US-237425P.
2000US-237604P.
2000US-237604P.
2000US-237608P.
2000US-237608P.
2000US-237608P.
2000US-237608P.
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2000US-235720P.
2000US-235840P.
2000US-235863P.
2000US-236028P.
2000US-236032P.
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2000US-234052P.
2000US-234509P.
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2000US-235077P.
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RESULT 26
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping; genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy; human immunodeficiency virus 1; single nucleotide polymorphism; SNP; chromosome 3p21.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
The invention relates to genetic variants of human chemokine (C-C motif) receptor 3 (CCR3) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the CCR3 gene in an individual Polynucleotides of the invention are useful for studying the expression
                                                                                                          WPI; 20
P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chemokine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carcinoma, papillary carcinoma
                                                                             Isolated (CCR3) ge
                                                                                                                                       Choi
                                                                                                                                                                                                18-MAY-2001; 2001WO-US16278
                                                                                                                                                                                                                                                                            variation
                                                                                                                                                                                                                                                                                                          variation
                                                                                                                                                                                                                                                                                                                                                                             variation
                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                Example
                                                                                                                                                                              18-MAY-2000;
                                                                                                                                                                                                                     22-NOV-2001.
                                                                                                                                                                                                                                       WO200187908-A2
                                                                                                                                                                                                                                                                                                                                                                                                          variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAR-2002
                                                                                                                                                          (GENA-)
                                                                                                                                      JΥ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
                                                                                                          2002-055681/07.
)B; AAE15320.
                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                  ed polymorphic variants of chemokine (C-C motif) receptor 3 gene useful for studying function of CCR3, expressing the CC n and to screen drugs to treat CCR3 activity-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
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                                                                                                                                                          GENAISSANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                      Kazemi A,
                                               Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                             2000US-205191P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                ۲,
                                                                                                                                                                                                                                                                                                                                                                                                replace
/*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (C-C
                                                                                                                                                                                                                                                        /standard_name= "Single
replace (1256, C)
/*tag= e
/standard_name= "Single
                                                                                                                                                                                                                                                                                                                                               /standard_name= "Single nucleotide 205..1272
                                                                                                                                                                                                                                                                                                                                                                             replace
                                                                                                                                                                                                                                                                                                                                                                                       /standard
                                                                                                                                                                                                                                                                                                                             /*tag= c
/product= "Human
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA; 1717
                                                                                                                                                          PHARM INC.
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                                                                                                                                       Koshy B;
                                                English
                                                                                                                                                                                                                                                                                                                                                                             (197, A)
                                                                                                                                                                                                                                                                                                                                                                                      name= "Single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor 3 (CCR3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 6.3;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Wilm's tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351
                                                                                                                                                                                                                                                                                      "Single nucleotide
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                                                                                                                                                                                                                                                                                                                   corresponds
                                                                                                                                                                                                                                                                                                                             protein'
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                                                                                                                                                                                                                                                           nucleotide
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                                                                                                                                                                                                                                                                                        (SNP) "
                                                                                                                                                                                                                                                                                                                                                           " (SNP)
                                                                              CCR3
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RESULT 27
AAD25245/c
ID AAD252
XX
AC AAD252
XX AC AAD252
XX Human
XX Human
XX Human
XX Human
XX Homo s
XX Key
FH Key
FT misc_f
FT T misc_f
FT T Tololol
XX WD1;
ZX WD1;
ZX WD1;
ZX Choi J
XX CHOA-
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and function of CCR3 and in expressing CCR3 proteins for use in screening candidate drugs to treat diseases related to CCR3 activity. They are also used in gene therapy. The polymorphism and haplotype data is useful for validating whether CCR3 is a suitable target for drugs to treat type IV hypersensitivity reactions and human immunodeficiency virus (HIV)-1, screening for such drugs and reducing bias cells in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for improving the efficiency and outcome of several steps in the discovery and development of drugs for treating diseases associated with CCR3 activity such as type IV hypersensitivity reactions and HIV-1. The present sequence is human CCR3 gene located on chromosome 3p21.3.
                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chemokine (C-C motif) receptor 3; CCR3 gene; haplotyping; genotyping; type IV hypersensitivity reaction; HIV-1; gene therapy; human immunodeficiency virus 1; polymorphism; chromosome 3p21.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human chemokine
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                                                                                                                                                                                                                        WO200187908-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Isolated polymorphic variants of chemokine (C-C motif) receptor
                                                                                                                                                         18-MAY-2001; 2001WO-US16278.
                                                                                                                           18-MAY-2000; 2000US-205191P.
                                                                                                                                                                                           22-NOV-2001
                               WPI; 2002-055681/07
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                                                                                             GENAISSANCE PHARM INC
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                                                             Kazemi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                     site (PS)
1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/note= "This degenerate base represents polymorphic
site (PS) 4"
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/note= "This degenerate
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/note= "This
                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "This
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                                                              Koshy
                                                               В,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                degenerate base represents polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                             degenerate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3;
                                                                                                                                                                                                                                                                                                                                    base
                                                                                                                                                                                                                                                                                                                                                                                                                                                             base represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 1717;
                                                                                                                                                                                                                                                                                                                                 represents polymorphic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             polymorphic
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RESULT 28
AAT85162/c
ID AAT85
XX
AC AAT85
AC AAT85
XX
DE Humar
XX
Chemc
KW Chemc
KW G pro
KW G pro
XX
FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT YX
PN W0971
XX
PD 26-JI
XX
PD 27-JI
PR 20-DI
XX
PD 27-JI
PR 20-DI
XX
PN WPI;
DR P-PSI
XX
PT Lo m
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PT to m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to genetic variants of human chemokine (C-C motif) creceptor 3 (CCR3) gene. The invention also relates to compositions and methods for haplotyping and/or genotyping the CCR3 gene in an individual. Polymucleotides of the invention are useful for studying the expression cc and function of CCR3 and in expressing CCR3 proteins for use in screening cc used in gene therapy. The polymorphism and haplotype data is useful for validating whether CCR3 is a suitable target for drugs to treat type IV hypersensitivity reactions and human immunodeficiency virus (HIV)-1, screening for such drugs and reducing bias cells in clinical trials of such drugs. The genotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for determining whether an an individual has one haplotype or haplotype pairs. The haplotyping method is useful for determining whether an individual has one haplotype or haplotype pairs. The haplotyping method is useful for improving the efficiency and outcome of several steps in the discovery and development of drugs for treating diseases associated with CCR3 activity such as type IV hypersensitivity reactions and HIV-1.

The present sequence is human CCR3 gene located on chromosome 3p21.3.
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Best Local S
Matches 19
New nucleic acid encoding chemokine receptors 88-2B and 88C - to modulate leukocyte trafficking, e.g. for treatment of inflammation, tumours, viral infections, autoimmune diseases,
                                                                                  WPI; 1997-341689/31.
P-PSDB; AAW27124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemokine receptor 88-2B; atherosclerosis; rheumatoid arthritis; tumour; asthma; viral infection; AIDS; inflammation; autoimmune disease; therapy; diagnosis; leukocyte trafficking; G protein coupled receptor; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human chemokine receptor 88-28 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1717 BP; 434 A; 427 C; 350 G; 502 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CCR3) gene useful for studying function of CCR3, expressing the CCI protein and to screen drugs to treat CCR3 activity-related diseases
                                                                                                                                                                                                                                 07-JUN-1996;
20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                     26-JUN-1997
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                                                                                                                                                Gray PW,
                                                                                                                                                                                                                                                                                               20-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                          (ICOS-)
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                                                                                                                                                                                                                                 96US-0661393
95US-0575967
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Pred. No.
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RESULT 29
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Matches 19
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                                                                                                                          New ovary polypeptides useful for detecting, diagnosing, monitoring, treating, staging and imaging cancers in humans having cancer and non-cancerous ovary disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                        The present invention provides human proteins and coding sequences specifically found in ovary cells. These can be used in the diagnosis treatment of ovarian diseases, including cancer. The present sequence
                                                                                                                                                                                                                                                                                                                                                            WO200240720-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABT04010 standard; DNA; 3426
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-SEP-2002 (first
                                                                                                 Claim 1; Page 162-164; 296pp; English
                                                                                                                                                                                                                                                                                                                                 23-MAY-2002
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                                                                                                                                                                                                                                           (DIAD-) DIADEXUS INC.
                                                                                                                                                                                                                                                                        20-NOV-2000; 2000US-249997P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovary specific coding sequence SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ovary;
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  3426
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                           sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ovarian
BP; 1107 A; 828 C; 714 G;
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                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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 777 T; 0 other;
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Query Match
Best Local Similarity

100.0%;

Score Pred.

NO;

6.9;

DB 24;

Length 3426;

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RESULT 30
AAF21269/c
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     cc oligonucleotides and compositions (I) comprising them. In the antisense (C) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the cexpression and or activity of target polypeptides associated with cativating peptide factors and malignancies, such as stimulating and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adhesion molecules and their receptors, cytokines and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system creceptors, defensins, growth factors, vasoactive peptides and considered specific antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or bronchoconstriction which are associated with a disease or condition aslacred from pulmonary vasoconstriction inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                            Low adenosine (A) content antisense oligonucleotides which trigger adenosine receptors during metabolism, useful e.g. cancers and respiratory obstructions -
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                                                                                                                                                                                                                                                                                                                                                             The present invention describes low adenosine
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 1183-1184; 1592pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-679539/66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyce JW;
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J W.
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RESULT 31
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XX Human
XX Human;
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Best Local (
The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                     New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYEC-) UNIV
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                                                                                                                                                                                                                                                                                            Disclosure;
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19; Conserv
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                                                                                                                                                                                                                                                                                         Page 1103-1104; 1343pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAST CAROLINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0095212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA; 3958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No.
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RESULT 32
AAT93601/c
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Matches
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                                                                                                                                                 17-JAN-1997;
26-APR-1996;
26-APR-1996;
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                                                                                                                                                                                                                                                                                                                                            SdC
                                                           P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eosinophil eotaxin receptor; CC CKR3; human; treatment; dermatitis; atopic condition; allergic rhinitis; conjunctivitis; bronchial asthma;
                                                                                               Daugherty BL,
                                                                                                                                                                                                    24-APR-1997;
                                                                                                                                                                                                                             06-NOV-1997.
                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              beta-chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human eosinophil eotaxin receptor CC CKR3 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3958 BP; 939 A; 1025 C; 855 G;
                                                                                                                                                                                                                                                      WO9741154-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT93601;
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                                                           1997-549685/50.
DB; AAW31850.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA;
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                                                                                                                                                 97GB-0000894.
96US-0016158.
96US-0017113.
                                                                                                 Demartino
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                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor; viral infection;
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/product= "human
4655..5099
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           /note= "5' genomic DNA flanking
3587..4654
                                                                                                                                                                                                                                                                              note= "terminator region'
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                                                                                                                                                                                                                                                                                                                                                       sequence"
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New isolated human eosinophil eotaxin receptor - used to develop products for treating and preventing atopic conditions e.g. aller rhinitis, dermatitis, conjunctivitis and bronchial asthma

allergic

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RESULT 33
ABZ68879/c
ID ABZ688
XX ABZ688
XX ABZ688
XX VICTOR
DE Nucleo
XX Human;
KW FSV in
XX FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT TOPI-
XX MO2003
XX PO 20-FEB
XX Homo 8
XX MO2003
XX PD 20-FEB
XX Homo 8
XX MO2003
XX PD 20-FEB
XX Homo 8
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA encodes a human eosinophil eotaxin receptor. This 5099 base pair sequence comprises a 1065 base pair open reading frame encoding a 355 amino acid eosinophil eotaxin receptor protein, flanked by a 5' genomic DNA sequence and a 3' terminator region. This novel eosinophil eotaxin receptor is a human beta-chemokine receptor designated CC CKR3. Agents which bind to this eosinophil eotaxin receptor can be used for the treatment and prevention of atopic conditions such as allergic rhinitis, dermatitis, conjunctivitis and bronchial asthma. Agents which block this eosinophil eotaxin receptor can be used to prevent viral infection in healthy individuals and slow or halt viral progression in the forted participation.
The present sequence encodes human chemokine receptor CCR3. The specification describes a method for modulating viral infection of a cell. the method comprises modulating a binding interaction between a cell chemokine-receptor and a surface protein of the virus. The proviso is that the cell chemokine-receptor is not CX3CR1 and that the
                                                                                                                                         Modulating viral infection of a cell, for treating or preventing respiratory virus infections, bronchitis, pneumonia or asthma, by modulating a binding interaction between a cell chemokine-receptor a surface protein of the virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chemokine receptor; CCR3; viral infection; surface protein; respiratory virus infection; respiratory syncytial virus infection; RSV infection; bronchiolitis; bronchitis; pneumonia; asthma; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of human chemokine receptor CCR3
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                                                                                                         Disclosure; Page 84-88; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-2002; 2002WO-CA01248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003014153-A2
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)B; ABP97726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 4015..5082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "CCR3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA;
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No. 7.3;
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                                                                                                                                                            cell chemokine-receptor
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CTGGGCCATCAGTGCTCTG

Conservative

Gaps

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RESULT 34
ABA63970/c
ID ABA63970 standard; D
XX
AC ABA63970;
XX
DT 01-FEB-2002 (first
XX
DT 01-FEB-2002 (first
XX
DE Human foetal liver s
XX
EN Human; foetal liver;
XX
OS Homo sapiens.
XX
PN W0200157277-A2.
XX
PN 09-AUG-2001; 2000US-
PR 26-MAY-2000; 2000US-
PR 26-MAY-2000; 2000US-
PR 27-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 03-AUG-2000; 2000US-
PR 03-AUG-2000; 2000US-
PR 03-AUG-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 04-OCT-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 30-JUN-2000; 2000US-
PR 21-SEP-2000; 2000US-
PR 26-MAY-2000; 2000US-

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Query Match
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Matches 18
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Matches
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                       The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virus is not HIV. The method is useful for treating or preventing respiratory virus infection in vertebrates, more particularly respiratory syncytial virus (RSV) infections, and related diseases, e.g. bronchiolitis, bronchitis, pneumonia or asthma.
                                                                                                Sequence 549 BP; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid probe; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes ing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
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                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
                        91.6%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                A; 148 C; 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
  0
  Score 17.4; D
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB
Pred. No. 7.4
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                  Ģ
                                                                                                  96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.4;
                                                                                                T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 25;
                                                 DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe
                                               22;
  1;
                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5791;
                                               Length 549;
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #12275
                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     umeful
    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
    0
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RESULT 35
ABA31145/c
ID ABA311.
XX ABA311.
XX ABA311.
XX ABA311.
XX ABA311.
XX Probe
XX Probe
XX Human;
XX Congen
XX Homo 8
XX Homo 8
XX WO2001
XX O9-AUG
XX O9-AUG
XX O9-AUG
XX O1-FEE
PR 04-FEE
PR 26-MAY
PR 30-JUN
PR 30-JUN
PR 30-JUN
PR 30-JUN
PR 27-SEI
PR 04-OCJ
XX WPI; ;
XX WPI; ;
XX Claim
XX Clai
AAK12471/c
ID AAK124
XX
XX
,AC AAK124
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                                                                                                   RESULT 36
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Best Local S
                                                                                                                                                                                                                                                                             Matches
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA31145 standard; DNA; 549
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001
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     AAK12471;
                                                    AAK12471 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #9611
                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                        549 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGGCCATGAGTGCTCTG
                                                                                                                                                                             CTGGGCCATGAGTGCTCTG
                                                                                                                                                                                                              CTGGGCCATCAGTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid probes
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DK,
                                                                                                                                                                                                                                                                                                                                                                    127 A; 148 C; 178 G; 96 T; 0 other;
                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9611;
                                                                                                                                                                                                                                                                                              91.6%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression analysis in human heart cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen
                                                    549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB.
                                                    ВP
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                        19
                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                              Score 17.4;
Pred. No. 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DR;
                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                         549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probe;
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart. The
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
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09-AUG-2001.

WO200157276-A2

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RESULT 37
AAK38179/c
ID AAK381
XX
AC AAK381
XX
DT 06-NOV
XX
DE Human
XX
Human;
KW microa
XX
OS Homo s
XX
PN WO2001
XX
PD 09-AUC
                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy and invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
                                                                                        microarray;
                                                                                                       Human; bone marrow expressed exon;
                                                                                                                                                                                               AAK38179;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   brains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-NOV-2001
                                                                                                                                                                  06-NOV-2001
                                                                                                                                                                                                                           AAK38179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                      101
                                                           sapiens
                                                                                                                                     bone
                                                                                                                                                                                                                                                                                                                               1 creeccarcaerecrere 19
                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      549
                                                                                                                                                                                                                                                                                                    CTGGGCCATGAGTGCTCTG 83
                                                                                                                                                                                                                             standard; DNA; 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                     marrow expressed single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 12462; 650pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed single
                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312.
2000US-0207456.
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                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                        expressed exon; gene expression analysis; probe; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                          91.6%;
94.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                     A; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                          Score 17.4; D
                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                     C; 178
                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank
                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probe SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                       96
                                                                                                                                    probe
                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0
                                                                                                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                        other;
                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                        NO: 12736.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                            549;
                                                                                                                                                                                                                                                                                                                                                               0
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RESULT 38
AAI18973/c
ID AAI18973;
XX
AC AAI18973;
XX
DT 12-OCT-201
XX
DT 12-Oct-201
XX
Cervical (
XX
OS Homo sapi(
XX
OS HO
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Best Local S
Matches 18
                                                                                                       04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 549
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26-MAY-2000;
                                                                                                                                                                                                                                                                                    30-JAN-2001; 2001WO-US00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
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                                                                  MOLECULAR DYNAMICS INC.
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                        Hanzel
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2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for gene expression analysis in human cervical cell sample.
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2000US-0207456.
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94.7%;
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Pred. No. 35
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RESULT 39
AAI44108/c
ID AAI441
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AC AAI441
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AC AAI441
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Probe;
XW Probe;
XW Probe;
XW Probe;
XW Geneti
XX
PN WO2001
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PPN WO2001
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PPR 30-JAN
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PPR 30-JAN
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PPR 26-MAY
PPR 26-MAY
PPR 27-SEF
PR 30-JUN
PR 27-SEF
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Matches 18
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI44108 standard;
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zing gene expression in
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                                                                                                                                                                                                                                                                                 Hanzel
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2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.

2000US-0024263.
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94.7%;
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n human placenta -
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Pred. No. 35;
                                                                                                                                                                                                                                                                                   Rank
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RESULT 40
ABS37802/c
ID ABS37
XX ABS37
XX ABS37
XX ABS37
XX 25-FI
XX ABS37
XX Humai
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Best Local S
Matches 18
                                                  The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention.

Conte: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
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ABS37802 standard; DNA; 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver \boldsymbol{\cdot}
  Sequence 549 BP; 127 A; 148 C; 178 G; 96 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 12792; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US00664.
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Query Match Best Local Similarity

91.6%; 94.7%;

Score 17.4; DB 23; Length 549; Pred. No. 35;

Search completed: January 13, 2004, 18:02:40 Job time : 124.5 secs

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Minimum
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Copyright (c) 1993 - 2004 Compugen Ltd
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BF884753
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BF884753 PM3-ET020
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ALIGNMENTS

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RESULT 1
BF884753
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS TITLE 299 bp mRNA linear PM3-ET0207-271200-003-e12 ET0207 Homo sapiens cDNA, BF884753 Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 299) Simpson, A.J. Homo sapiens BF884753.1 Homo sapiens (human) GI:12275402 mRNA sequence.

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BM146496/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0207-271200-003-e12&t3=2000-12-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 354)
1 (bases 1 to 354)
Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman,F.R. Jr.,
Gunaratne,P.H., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM146496 354 bp mRNA linear EST 30-NOV-2001 TCAAP1E4963 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP4963, mRNA
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Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                      Tel: 832-824-4536
Fax: 832-825-4038
                                                                                                                                                                                                                                                                                                                                                         at Baylor College of Medicine 1102 Bates, MC3-3320 Houston,
                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dr. Judith F. Margolin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BM146496
BM146496.1 GI:17165472
                                                                                                                                                                                                                                                     Email: clones@txccc.org
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                            Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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/clone_lib="ET0207"
/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
/note="Organ: lung_tumor; Vector was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
100 stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="leukopheresis"
/cell_type="myeloid cell"
/dev_stage="pediatric 6 years"
                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TCAAP4963"
                                                                               sex="male"
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                                                                                                                                                                                                                                                                                                                                                           TX 77030, USA
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REFERENCE
AUTHORS
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ORGANISM
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BF986303/c
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Simpson,D.H., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF986303 357 bp mRNA linear QV4-GN0144-031000-446-bl0 GN0144 Homo sapiens cDNA,
                                                                                                                                                                                                                             This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV4&t2=QV4-GN0144-031000-446-b10&t3=2000-10-03&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF986303
                                                                                                                                                                                                   Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence tags
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                                                                                                             quality sequence start: 5 quality sequence stop: 357 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA"

/note="Vector: lambda pSB; Site 1: BamHI; Site 2: EcoRI; First strand cDNA was primed with an anchored XhoI-oligo(dT) primer [5'GGAGGACTCGAGCGCGCAGGAGGAG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGGAGCTCGGATCCGCGCAGGATCATAATAATAAT(C) 3'].
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.8e+02;
; Mismatches 0;
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BU431613/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                        19;
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1 (bases 1 to 478)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
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478 bp mRNA linear EST 09-SEP-2002 UI-HF-BNO-afr-f-04-0-UI.rl NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3067902 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                          /cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_50"
/clone_lib="NIH_MGC_50"
/clone_"Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Ec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:3067902"
/tissue_type="lymph"
/cell_type="germinal center B cells"
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mol_type="mRNA"
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Pred. No. 3.8e+02;
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SOURCE **ŒYWORDS**

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JOURNAL
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Matches 19; Conserv
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                                                                                                                      BX359469 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO57YHO2 5-PRIME, mRNA sequence.
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CB961169.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 785)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT 13762074 NIH MGC 147 Homo
IMAGE:30344148 5', mRNA sequence.
CB961169
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                             GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30344148"
/tissue_type="Human Placenta"
/lab_host="DH10B_TonA"
/clone_lib="NIH_MGC_147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH MGC library."

a 257 c 234 g 140 t
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                                                                                                      GI:30382361
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19; DE 100.0%; Pred. No. 4.2 cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  DB 14;
4.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 785;
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                                                                                                                                                                                         EST 05-MAY-2003
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REFERENCE
AUTHORS
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AUTHORS
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VERSION
KEYWORDS
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H31083/c
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ORIGIN
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MEDLINE
PUBMED
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                               1 (bases 1 to 209)
1 (bases 1 to 209)
Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.C.
Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H31083.1 GI:976505
EST.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgi-bin/cluster.cgi?seq=CSODI057DD01QP1&cluster=10421.f. Contact Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI057DD01QP1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10421.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                              Other_ESTs: EST104773
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST104774 Rat PC-12 cells, untreated Rattus 5' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: nhlee@tigr.org
For clone availability please contact
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
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                                                                                 Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                        factor treatment
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 336 c 293 g 204 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="CS0DI057YH02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 19; DB 13;
Pred. No. 4.3e+02;
); Mismatches ~ 0;
                                                                                                                                                                                                                                                                92,
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                                         the TIGR Database
                                                                                                                                  20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
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JOURNAL COMMENT
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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DEFINITION
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ORIGIN
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BB306760/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Shiraki, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshiraki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB306760 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B230209H01 3' similar U79774 Mus musculus NNP-1 var (NNP-1) mRNA, mRNA sequence.
                                                                                                 Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB306760
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB306760.1 GI:9007465
                                                                                                                                                                                                                                                                                                                                                                                           Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Mouse ESTs (Konno, H., et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
1 (bases 1 to 266)
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                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
xhoI; poly(A) + RNA was purified from untreated PC12 cells
cultured for 9 days. cDNA was constructed using an
oligo-dT primer and directionally cloned using the Lambda
ZAP II Vector Kit by Stratagene"

61 c 51 g 49 t
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/db_xref="ATCC (inhost):2000079"
/db_xref="taxon:10118"
/clone="RPCAB19"
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94.7%;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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DEFINITION
ACCESSION
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BQ331140
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1 (bases 1 to 318)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Nagai, M.A., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Goldman, G.H., Carvalho, A.F., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            μ
Rua Prof.
Brazil
                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                            BQ331140 318 bp mRNA linear PM3-ET0207-151200-001-b02 ET0207 Homo sapiens cDNA, BQ331140 GI:20972150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                            Simpson, A.J
                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                         Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, adult male corpora
quadrigemina"
                 Antonio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
mol_type="mRNA"
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dev_stage="adult"
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                                                                                                                           Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ified pBluescript KS(+) after bulk excision from Lambda
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94.7%;
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Pred. No. 1.8e+03;
0; Mismatches 1
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               4 andar, 01509-010,
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RESULT 10
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                                                         Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu
Cligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 35-133,

>GC_rich#Low_complexity 158-225, >(CGGG)n#Simple_repeat 320-354,

>GC_rich#Low_complexity
                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE102744 355 bp mRNA linear IUI-R-BT1-aqp-f-05-0-UI.s1 UI-R-BT1 Rattus norvegicus UI-R-BT1-aqp-f-05-0-UI 3', mRNA sequence.
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18; Conserv
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                                                                                                                                                                                                                                                                                                        Coordinated Laboratory
                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                 8889548
                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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Bonaldo, M.F., Lenno
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                                     Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
                      POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-ET0207-
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/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
/note="Organ: lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
2 others
Location/Qualifiers
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/db_xref="taxon:9606"
/dev_stage="Adult"
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Pred. No. 1.8e+03;
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RESULT 11
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AUTHORS
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Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA892154
386 bp
EST195957 Normalized rat kidney,
RKIAN02 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                           Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 386)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA892154.1
                                                                                                                                                                                                                                                                       Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-BT1"
/clone_lib="UI-R-BT1"
/clone_lib="UI-R-BT1"
/clone_lib="UI-R-BT1"
/clone_lib="UI-R-BT1"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
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/db_xref="taxon:10116"
/clone="UI-R-BT1-aqp-f-05-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technolo
                                                                                                                                          /organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2017749"
/db_xref="taxon:10118"
/clone="RKIAN02"
                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                        /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
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91.6%;
94.7%;
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Pred. No. 1.8e
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Score 17.4; DB 9;
Pred. No. 1.8e+03;
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                Length 386;
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sp. cDNA clone
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CB735745/c
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CB735745
CB735745.1 GI:29802948
                                                                                                                                                                                                                               573 bp mRNI
AMGNNUC:NRDG1-00012-A1-A nrdg1 (10855)
nrdg1-00012-a1 5', mRNA sequence.
CB614996
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Chordata;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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           One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
                                                                                 Amgen EST Program.
Amgen Rat EST Program
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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Amgen EST Program
Amgen Rat EST Program
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                                        Amgen, Inc
                                                     Contact: Dan Fitzpatrick
                                                                                                                                                                                                                   CB614996.1 GI:29574884
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Plate: 00012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="W Rat hypothalamus (10464)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; W
/nypothalamus adult female Wistar rat avg. insert size
kb fraction 6 and 7"
119 c 103 g 103 t 61 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy4-00032-b2"
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Pred. No. 1.9e+03;
0; Mismatches 1
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AZ952841.1
GSS.
Mus musculus
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1 (bases 1 to 580)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: |
Plate: 0217 row: N column: 18
Peq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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S80 bp DNA line 2M0217N18R Mouse 10kb plasmid UUGC2M library Mu clone UUGC2M0217N18 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Utah C
University of Utah
Rm. 308, Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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             /lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through &
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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165 c 149 g
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/clone_lib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: Sall; Site_2: Not1; rat
                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="nrdg1-00012-a1
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                                                                                                                                                                                                                        db_xref="taxon:10090"
clone="UUGC2M0217N18"
                                                                                                                                                                                                       sex="Female"
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94.7%;
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kinase. Adaptor oligonucleotides were
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1837 row: 1 column: 19 High quality sequence stop: 349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1077)

1 (bases 1 to 1077)

NAIH-MGC http://mgc.nci.nih.gov/.

NAIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: Location/Qualifiers
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Tissue Procurement: ATCC
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             /lab host="DH108 (phage-resistant)"
/clone lib="NIH_MGC 17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 388 c 340 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ligated to the blunt ends in high molar excess. The
                                                                                                                                                                                                                                                                                                           'mol_type="mRNA"
'db_xref="taxon:9606"
'clone="IMAGE:5020578"
                                                                                                                                                                                                                                                                              tissue_type="rhabdomyosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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94.7%;
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Pred. No. 1.9e+03;
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Query Match
Best Local Similarity
Matches 18; Conserv

Conservative

0;

91.6%; 94.7%;

Score 17.4; DB 12; Pred. No. 2.1e+03; 0; Mismatches 1;

Length

0

Gaps

0

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RESULT 16
BQ059970/c
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BE887786/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2072 row: h column: 18
High quality sequence start: 19
High quality sequence start: 19
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   1115
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BE887786 1562 k
601511359F1 NIH_MGC_71 Homo samRNA sequence.
BE887786
BE887786.1 GI:10343430
EST.
Homo sapiens (human)
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5', mRNA sequence.
BO050070
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1 (bases 1 to 1164)

NIH-MGC http://mgc.nci.nih.gov/.

NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:5816129"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_99"
/clone_lib
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/mol_type="mRNA"
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94.7%;
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                                                                                                                                                                                          1562
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                                                                                                                                                         sapiens
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                                                                                                                                                                                            mRNA
                                                                                                                                                         cDNA clone IMAGE:3912590
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AK031524
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Mammalia; E
                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK031524 3874 bp mRNA linear HTC 05-DEC-2002 Mus musculus 13 days embryo male testis cDNA, RIKEN full-length enriched library, clone:6030447F10 product:hypothetical protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consorthtp://image.llnl.gov
Plate: LLAM9731 row: f column: 15
High quality sequence stop: 6.
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1 (bases 1 to 1562)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Shibata, K., Itoh, M., Aizawa, K., Konno, H., Akiyama, J., Nishi, K., Sumi, N., Ishii, Y., Nakamura, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                               HTC; CAP trapper.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AK031524.1 GI:26327378
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                                                                                                                                                                                                                                                                                                       High-efficiency
                                                                                                                                                                                                                                                                                                                            Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                11042159
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                                                                                                                                                                                                                                                                                                                                                                                                                             musculus (house mouse)
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                                                                                                                                                                                                                                                                                     Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. " 579 c 208 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3912590"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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94.7%;
                                                                                                                                                                                                                                                                                     full-length cDNA cloning
303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
 Nagaoka,S., Sasaki,N., C
Kitsunai,T., Tashiro,H.,
Hazama,M., Nishine,T., H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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                                                                                                                                            of new genes
                                          Carninci, P.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

AL Nature 420, 563-573 (2002)

E 6 (bases 1 to 3874)

RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                   cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in R
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                                                                                                                       URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                               prepare mouse tissues.
Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                  Division of Experimental Animal Research in Riken contributed to
/organism="Mus musculus"
/mol_type="mRNA"
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pacs1-60_4515, genomic survey sequence.
BZ554088
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Box 352145, Seattle, WA 98105-2145,
Tel: 2062216954
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Spencer, D.H., Raymond, C.K., Smith,
Burns, J.L., Kaul, R. and Olsen, M.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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/mol_type="genomic DNA"
/strain="1-60"
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/clone_Tib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
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/note="clinical isolate 1-60 Whole genomic shotgun
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                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 214)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy ProTumor Gene Index
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1 (bases 1 to 206)
0gihara, Y. and Murai, K.
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Triticum aestivum
                             Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                  hh37g01.x1 NCI_CGAP_Co14
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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EST.
Tissue Procurement: Christopher Moskaluk, Emmert-Buck, M.D., ph.D.
                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                    mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="seed DPA10"
/dev_stage="Feekes' scale 11.2"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_e"
46 c 79 g 44 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No. 4.5e+03;
0; Mismatches 1
                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                      214 bp mRNA linear EST 23-MAR-2000 Homo sapiens cDNA clone IMAGE:2957328 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
               M. D.,
                                                                                                                                           Hominidae;
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                 Ph
                                                                                              Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                               206;
              .D.,
                                                                                                                                                          Euteleostomi;
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                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                 Michael
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                                                                                              (CGAP)
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REFERENCE
AUTHORS
TITLE
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AJ460522/c
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KEYWORDS
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Best Local S
Matches 17
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Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                              Institute of Biotechnology University of Helsinki P.O.Box 56 (Viikinkaari 6A), Finland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AJ460522 240 bp
AJ460522 S00002 Hordeum vulgare
                N
                                                                                                                                                                                                                                                                                                                                                       Barley EST's
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 240)
Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            АJ460522.1
EST.
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                                                                                                                                                                                                                                                                                                                                            Contact: Schulman AH
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                                                          Similarity
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GGTCTGCAGCGGGATGGT
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Col4"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Saana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2957328"
                                                                                                                                                                                                                                       organism="Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="moderately-differentiated adenocarcinoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:21059442
                                                          86.3%;
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Pred. No. 4.
                                                            Score 16.4; DB 9;
Pred. No. 4.6e+03;
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GGTCTGGAGCGGGATGGT 175

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RESULT 24
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AUTHORS
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BJ293359/c
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                                                                                                                                       AUTHORS
TITLE
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                                                                                                                  Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
; Triticeae; Triticum.
1 (bases 1 to 284)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
                                                  Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
17; Conserv
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
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Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
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                                                                                                                                                                                                                                                                                                                     aestivum cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Triticeae; Triticum.
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                                                                                                                                                                                                                                                                                                                  284 bp
Y. Ogihara unpublished cI
cDNA clone whsl32119 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="seed DPA30"
/dev_stage="Feekes' scale 11.3"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_
90 c 74 g 41 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whsl31117"
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94.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 4.6e+03;
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                                                   411-8540, Japan
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cDNA library, Wh_SL
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Triticum
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Triticum
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aceae; Pooideae
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RESULT 26
CA644225
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AUTHORS
TITLE
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VERSION
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BJ299963
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Matches 17
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CA644225 292 bg wre1n.pk0078.hl wre1n Triticum 5' end, mRNA sequence.
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1 (bases 1 to 292)

Ogihara, Y. and Murai, K.

Expressed genes in Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BJ299963 Y. Ogihara unpublished cDNA library, Wh_SL Triticum aestivum cDNA clone whsl32n06 3', mRNA sequence.
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                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                               Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum (bread wheat)
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                                                                                                                          GGTCTGCAGCGGGATGGT 19
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                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                 /tissue_type="seed_DPA30"
/dev_stage="Feekes' scale 11.3"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_SL"
82 c 105 g 58 t 2 others
                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="seed DPA30"
/dev_stage="Feekes' scale 11.3"
/clone_lib="Y. Ogihara unpublished
67 c 101 g 59 t 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whs132119"
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                                                                                                                                                                                                                                                                                           clone="whs132n06"
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Pred. No. 4.7e+03;
0; Mismatches 1;
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                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                              1 (bases 1 to 324)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miao,G., Caraher,N. and nat
DuPont Wheat cDNA Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
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                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Scott V. Tingey
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                                                                                                           Proc. Natl.
                                                                                                                           sequence tags
                                                                                                                                             Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                        BI013302.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . I. DuPont de Nemours and Company Innovation Way, P.O. Box 6104, Newark, pl: 302-631-2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 292
Prof. Antonio Prudente 109, 4 andar, 01509-010,
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/tissue_type="root"
/clone_lib="wreln"
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Pred. No. 4.7e+03
D; Mismatches
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ET0154 Homo sapiens cDNA,
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BU974641/c
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Best Local
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 324.
Location/Qualifiers
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Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-ET0154-
                                                                                                                                                                                                                                                          Email: stein@ipk-gatersleben.de
Insert Length: 336 Std Error:
Plate: 28 row: J column: 24
                                                                                                                                                                                                                                                                                                                                           Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522
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BU974641
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HB28J24r BC Hordeum vulgare
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                                                                                                                                                                                                                                    Seq primer: Ml3rev
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chuk, V., Zhang, H., Weschke, W.,
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/clone lib="ET0154"
/note="Organ: lung_tumor; Vector: puc18; Site 1: SmaI;
/note="Organ: lung_tumor; Vector: puc18; Site 1: SmaI;
/note="Organ: lung_tumor; Vector: puc18; Site 1: SmaI;
/note="Organ: lung_tumor; Vector was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
83 c 112 g 75 t
                                                                                                                                                                                                              Location/Qualifiers
/tissue_type="developing caryopsis"
/dev_stage="8-15 DAP (days after pollination)"
/lab_host="XL10-Gold"
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'db_xref="taxon:9606"
'dev_stage="Adult"
                                                                                       'db_xref="GABI:239491"
'db_xref="taxon:112509"
                                                                                                                             cultivar="barke"
                                                                                                                                                                        organism="Hordeum vulgare
                                                               clone="HB28J24"
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94.4%;
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Pred. No. 4.8e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holma, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterst, R., Williamson, A., Wohldmann, P. and Wilson, R.

The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
Insert Size: 484
High quality sequence stops: 220
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 484 Std Error: 0.00
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Yh43f06.rl Soares placenta Nb2HP Homo sapiens
IMAGE:132515 5', mRNA sequence.
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17; Conserv
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Insert Length: 484
Seq primer: M13RP1
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Contact: Wilson RK
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Hillier,L., Clark,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:538127"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:132515"
                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                       sex="Female"
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Pred. No. 4.8e+03;
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LOCUS DEFINITION

AI473980 362 bp mRNA linear EST 09-MAR-tm04g09.xl NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2155648

EST 09-MAR-1999 NGE:2155648 3'

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AW769047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 355)
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AW7690
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17; Conserv
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH108"
/clone_lib="NCI_CGAP_Co14"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
a 101 c 111 g 63 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3005349"
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Pred. No. 4.8e+03;
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                                                                                                                                                                                                                                                                                                                        .8e+03;
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VERSION
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BF112016
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VERSION
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ORGANISM
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DEFINITION
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Best Local Similarity
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 197.
Location/Qualifiers
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Primates; Catarrhini; Hominic
1 (bases 1 to 369)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                               BF112016 369 bp mRNA 17137f04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo_IMAGE:3523711 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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BF112016.1
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40UP from Gibco.

Location/Qualifiers
                                                                                                  Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                             Email: cgapbs-r@mail.nih.gov
                                                                                                                                           Tumor Gene Index
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: nsert size 1.7 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2155648"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="moderately-differentiated adenocarcinoma"/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                              GI:10941629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.3%;
94.4%;
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                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                        Genetics (www.resgen.com).
Seq primer: M13 REVERSE.
                                                                                                                                                                                                                                                                                                                                    Coordinated Laboratory
University of Iowa
375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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Bonaldo,M.F., Lennon,G. and Sos
Normalization and subtraction:
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                                                                                                                                                                                                                                               Tissue Procurement: Dr.
                                                                                                                                                                                                                                                               Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                              8889548
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                                                                                                                                                 rissue Procurement: Dr. Gregg Hageman cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTCTGCAGCAGGATGG 330
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Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneIDs: Soares NbHSF pool 1: 309384-310919, 323208-325895 Soares NbHSF pool 1: 15032-147335, 147720-148103, 148872-149255, 15002 - 150407, 151176-152327 Soares Nb2HFP-9W pool 1: 758280-760583, 772104-774407 Soares NbHPA pool 1: 723720-726407, 739080-326863 Soares NbHOT pool 1: 723720-726407, 739080-740999 Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Soares NSF F8 9W OT PA P S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from five normalized
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96 c 123 g 91 t
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="IMAGE:3523711"
                                                                                    Location/Qualifiers
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94.4%;
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Pred. No. 4.8e+03;
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                                                                                                                                                                                                                                                                                                                                       MEBRF, Iowa City, IA 52242,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Soares, M.B.
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AW662148
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Best Local S
Matches 17
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TITLE
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                                                                                                                                                 source
                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life

Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The

I.M.A.G.E. Consortium DNA Sequencing by: Washington University

Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

Seq primer: -40UP from Gibco

High quality sequence stop: 233.

Location/Qualifiers
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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EST.
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382 bp mRNA linear EST 06-APR-2000 hi20b08.x1 NCI_CGAP_GUI Homo sapiens cDNA clone IMAGE:2972823 3' similar to TR:Q60997 Q60997 CRP-DUCTIN PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UI-E-EJI is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
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/lab_host="DH10B (Life Techno
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                              clone="IMAGE:2972823"
                                                           db_xref="taxon:9606"
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94.4%;
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pooled high-grade transitional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome (Clone distribution: NCI-CGAP clone distribution: found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 496 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham.
Location/Qualifiers
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1 GGGTCTGCAGCGGGATGG
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1 (bases 1 to 382)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                           /clone lib="NCI CGAP Co10"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo (N-Soares4). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NCI_CGAP_GU1"
/note="Organ: genitourinary tract; Vector: pCMV-SPORT6;
Site_1: SalI; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Library constructed by Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1144634"
                                                                                                                                                                                                                                                                                                                                                                         tissue_type="colon tumor RER+"
/lab_host="DH10B"
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                                                                                86.3%;
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94.4%; Pred. No. 4.8e+03;
tive 0; Mismatches 1
                                                               0
                                                                                Score 16.4; DB 9;
Pred. No. 4.8e+03;
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                                                                 Mismatches
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                                                                                                    Length 382;
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clone I
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IMAGE:1144634 3',
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BM443000/c
                                                                     SOURCE
ORGANISM
                                                                                                                        ACCESSION
VERSION
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International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
                                                                                                                                           EBro02_SQ002_C13_R root, 3 week, hydroponic g Optic, EBro02_Hordeum vulgare subsp. vulgare EBro02_SQ002_C13_S', mRNA_sequence.
            Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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Istituto Sperimentale per la Cerealicoltura
via San Protaso 302, I-29017 Fiorenzuola d'Arda (PC),
Tel: 39 0523 983758
Fax: 39 0523 983750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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394 bp mRNA linear EST ISC010.A09F990908 ITEC ISC Barley Leaf Library Hordeum subsp. vulgare cDNA clone ISC010.A09, mRNA sequence.
                                                                                                       BM443000 GI:21947654
BM443000.2 GI:21947654
EST.
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EST.
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BE411862
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                                                                                                                                                                                                                                                                                                                                     GGTCTGCAGCGGGATGGT 19
  (bases
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/dev_stage="first leaf, cold stress"
/clone_lib="ITEC ISC Barley Leaf Library"
/note="Vector: UNI-ZAP XR; 0.7-2.0 Kbp av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:112509"
/clone="ISC010.A09"
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94.4%; Pred. No. 4.90
cive 0; Mismatches
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low nitrogen, cv
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AUTHORS
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HC02F21y HC Hordeum vulgare subsp.
3-PRIME, mRNA sequence.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                               Molecular Markers Group, Department Genbank Institute of Plant Genetics and Crop Plant F Corrensstr. 3, 06466, Gatersleben, Germany Tel: 039482-5522 Fax: 039482-5595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Dynamics/Computational Biology Scottish Crop Research Institute
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Contact: Waugh
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                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                Email: stein@ipk-gatersleben.de
Insert Length: 402 Std Error:
Plate: 2 row: F column: 21
                                                                                                                                                                                                                                                                                                                                                                                    Contact: Stein Nils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Graner,A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Varshney, R.K., Zhang, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barley ESTs from coleoptile tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                              primer: SP6
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/clone="EBro02_SQ002_C13"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="root, 3 week, hydroponic grown, low nitrogen, /clone_lib="root, 3 week, hydroponic grown, low nitrogen, cv Optic, EBro02"
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Site_1: Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Sal I; Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Sal I; Sal I; Site_2: Not I;
/note="Vector: pSPORT1; Sal I; Sal 
Location/Qualifiers
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Waugh R, Marshall DF
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'cultivar="Optic"
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94.4%;
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Pred. No. 4.9e+03;
                                                                                                              Error:
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          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 39
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Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 192 row: M column: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Conter Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BH306574
BH306574.1 GI:17218982
GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., (A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH306574 403 bp DNA linear (CH230-192M6.TV CHORI-230 Segment 1 Rattus norvegicus
                                                                                                                                                                                                                                                                                               Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CH230-192M6, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 403)
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          106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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          þ
                  /cell_type="Brain"
/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/S8NH8d/MCW) BAC library produced by
Pieter_de_Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="6 and 10 hour drought stress by placing plants moist paper (75% rel. humidity) in light"

106 c 140 g 81 t
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                                                                                                                               /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-192M6"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Root"
/dev_stage="3 week old"
/clone_lib="HC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:112509"
/clone="HC02F21"
                                                                                                                                                                                                            organism="Rattus norvegicus"

mol_type="genomic DNA"
                                                                                                                                                                                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strain="cv tokak"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="GABI:549519"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Hordeum vulgare subsp. vulgare"
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94.4%;
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Jong"
77 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16.4; DB 14; Pred. No. 4.9e+03;
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KEYWORDS
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Best Local Similarity
                                                                                                                                     Matches
                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mi
M.D., Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing distribution: NCI-CGAP clone distribution info found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 498 Std Error: 0.00

Seq primer: -40UP from Gibco.
361
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                                                                 1 GGGTCTGCAGCGGGATGG 18
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1 (bases 1 to 406)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI492104.1
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                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                              /clone="IMAGE:2108041"
/tissue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%;
94.4%;
                                                                                                                                                                      86.3%;
94.4%;
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Pred. No. 4.9e+03;
0; Mismatches 1;
                                                                                                                                                                      Score 16.4; DB 9;
Pred. No. 4.9e+03;
                                                                                                                                     Mismatches
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sapiens cDNA
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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gn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
gn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
gn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
gn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
gn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
   112
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2 US-10-085-117-12

2 US-10-085-117-11

4 US-10-085-117-10

4 US-10-085-117-10

1 US-09-918-995-7315

3 US-10-183-708-49

3 US-10-183-708-49

3 US-09-738-626-109

1 US-09-738-626-109

1 US-10-027-632-6525

US-10-027-632-188580

US-10-027-632-188581

US-10-027-632-188581

US-10-027-632-188581
                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                        Description
                                          Sequence 12, Appl
Sequence 11, Appl
Sequence 546, App
Sequence 10, Appl
Sequence 7315, Ap
Sequence 49, Appl
Sequence 49, Appl
Sequence 109, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 6525, Ap
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US-09-815-242-7546 US-09-815-242-9877 US-10-339-604-35 US-10-339-604-36 US-09-983-965-731	525 761 574	US-10-429-802-28 US-09-016-8698-22 US-09-016-8698-21 US-09-908-671-1 US-09-984-664-15	PPPP	US-10-027 US-10-369- US-09-939-	US-10-029-3 US-10-027-6 US-10-027-6 US-10-027-	US-10-027-632-188583 US-10-027-632-188580 US-10-027-632-188581 US-10-027-632-188582 US-10-027-632-188583
Sequence 7546, Ap Sequence 9877, Ap Sequence 35, Appl Sequence 36, Appl Sequence 731, App	127	28, Ap 22, App 21, App 1, App 15, Ap	134	174763 44678, 1, Appl	0000	Sequence 188583, Sequence 188580, Sequence 188581, Sequence 188582, Sequence 188583,

ALIGNMENTS

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; SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 12; LENGTH: 2694; TYPE: DNA; ORGANISM: Homo sapiens
US-10-085-117-12
                                                                                                                           RESULT 2
US-10-085-117-11/c
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US-10-085-117-12/c
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Sequence 11, Application US/10085117
Publication No. US20030232334A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/10085117 Publication No. US20030232334A1 GENERAL INFORMATION:
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                  97 GGGTCTGCAGCGGATGGT 79
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1 Similarity 100.0%; Pred. No. 6.
19; Conservative 0; Mismatches
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; SEQ ID NO 10
; LENGTH: 36595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-10
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US-10-085-117-10/c
; Sequence 10, Application US/10085117
; Publication No. US20030232334A1
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; ORGANISM: Homo sapiens
US-10-085-117-11
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SEQ ID NO 546
LENGTH: 3439
TYPE: DNA
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Best Local Similarity 100.0%;
Matches 19; Conservative (
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                                                                                                PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                    APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
FILE REFERENCE: 529452000121
CURRENT APPLICATION: NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 361
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CURRENT APPLICATION NUMBER: US/10/085,117
CURRENT FILING DATE: 2002-02-27
                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 3420843CB1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          273
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Pred. No. 6.2;
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(390)
; OTHER INFORMATION: n = A,T,C or
US-09-918-995-7315
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                                                                       ; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Drosophila Melanogaster
US-10-183-708-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/10183708 Publication No. US20030143679A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserva
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                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7315
Query Match
Best Local Similarity
Matches 17; Conserv
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Best Local
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/932,227
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: US 09/257,706
PRIOR FILING DATE: 1999-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
                                                                                                                                                                                                                                                                                                              APPLICANT: VOSSHALL, LESLIE
APPLICANT: AMREIN, HUBERT
APPLICANT: AXEL, RICHARD
TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
FILE REFERENCE: 0575/58715-AA-PCT-US/JPW/ADM/BJA
CURRENT APPLICATION NUMBER: US/10/183,708
CURRENT FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 GGGTCTGCAGCTGGATGG 101
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94.4%;
                   86.3%;
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                   Score 16.4; DB 13; Pred. No. 1.2e+02;
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Pred. No. 1.4e+02
0; Mismatches
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     Mismatches
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                                     Length 1194;
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GGTCTGCAGCGGATGGT 19

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SOFTWARE: PatentIn version 3.0
SEQ ID NO 49
LENGTH: 1194
TYPE: DNA
ORGANISM: Drosophila Melanogaster
US-09-932-227-49
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                                                                                                                                                                                                                                       APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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                                                                                                                                                                                           SOFTWARE: PatentIn ver. SEQ ID NO 109
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                                                   Query Match
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APPLICANT: AMREIN, HUBERT
APPLICANT: AXEL, RICHARD
TITLE OF INVENTION: GENES ENCODING INSECT ODORANT RECEPTORS AND USES THEREOF
FILE REFERENCE: 0575/58715-A-PCT-US/JPW/ADM/BJA
CURRENT APPLICATION NUMBER: US/09/932,227
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: PCT/US00/04995
PRIOR FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 108
                                                                                                   ORGANISM: Corynebacterium glutamicum -09-738-626-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
                                                                                                                                                     LENGTH: 1824
TYPE: DNA
/ Match 86.3%; Score 16.4; DB 10; Length 1824;
Local Similarity 94.4%; Pred. No. 1.2e+02;
1es 17; Conservative 0; Mismatches 1; Indels 0;
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Local Similarity 94.4%;
hes 17; Conservative
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OCHIAI, KEIKO
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; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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US-10-029-386-14644
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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Best Local Similarity
Matches 17; Conserv
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14644, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                                            SEQ ID NO 14644
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                                                                                                                                                                                                                                                 APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL ITITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INFORMATION: MAP TO CHR22_166.0
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: SWISSPROT HIT: P32927, EVALUE 2.00e-16
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                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3309400
                                                                                                                                                                                                         ENGTH: 153
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TATEISHI, NAOKO
SENOH, AKIHIRO
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FOR GI

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; SEQ ID NO 6525
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-6525
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;

TITLE OF INVENTION: Polymorphisms in the Human Genome;

FILE REFERENCE: 108827.129;

CURRENT APPLICATION NUMBER: US/10/027,632;

CURRENT FILING DATE: 2002-04-30;

PRIOR APPLICATION NUMBER: US 60/218,006;

PRIOR APPLICATION NUMBER: US 60/198,676;

PRIOR APPLICATION NUMBER: US 60/198,676;

PRIOR APPLICATION NUMBER: US 60/193,483;

PRIOR FILING DATE: 2000-03-29;

PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-10-027-632-6525/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6525, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
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17; Conserv
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17; Conserv
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; LENGTH: 504
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-6525
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                                      RESULT 14
US-10-027-632-188581
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PRIOR FILING DATE: 1999-11-23;
PRIOR APPLICATION NUMBER: US 60/156,358;
PRIOR FILING DATE: 1999-09-28;
PRIOR APPLICATION NUMBER: US 60/146,002;
PRIOR PILING DATE: 1999-08-09;
NUMBER OF SEQ ID NOS: 325720;
NUMBER OF SEQ ID NOS: 325720;
SOFTWARE: FASCSEQ for Windows Version 4.0
Sequence 188581, Application US/10027632 Publication No. US20030204075A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Human
                                                                                                                                                                                                                                                                                                                               ENGTH: 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US 60/198,676
OR FILING DATE: 2000-04-20
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR APPLICATION NUMBER: US 60/167,363
OR APPLICATION NUMBER: US 60/167,363
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APPLICATION NUMBER: US 60/156,358
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17; Conserv
                                                                                                                                                          1 GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                83.2%;
89.5%;
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                                                                                                                                                                                                                  Score 15.8; DB 1
Pred. No. 2.7e+02
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Pred. No. 2
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                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                                   Length 507;
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GENERAL INFORMATION:

APPLICANT: Wang, David G. TITLE OF INVENTION: Ident TITLE OF INVENTION: Poly

Identification Polymorphisms

and Mapping of Single Nucleotide in the Human Genome

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Query Match
Best Local Similarity
Matches 17; Conser
GGGTCTGCAGCGGGATGGT 19
                                    83.2%;
                          Score 15.8; DB 13;
Pred. No. 2.7e+02;
                                              Length 507;
                            Indels
                            0
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188582
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188582
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; ORGANISM: Human
US-10-027-632-188581
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
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LENGTH: 507
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28 PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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CURRENT FILING DATE: 2002-04-30
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17; Conserv
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Pred. No. 2.7e+02;
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Gaps
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US-10-027-632-188580
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US-10-027-632-188583
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
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ORGANISM: Human
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Matches

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 188580
LENGTH: 507
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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89.5%;
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Pred. No. 2.7e+02
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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; ORGANISM: Human
US-10-027-632-188580
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US-10-027-632-188581
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US-10-027-632-188582
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US-10-027-632-188581
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GENERAL INFORMATION
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GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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les 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              18
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Pred. No. 2.7e
0; Mismatches
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Pred. No. 2.7e+02;
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; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: 188583
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-188582
                                                                           US-10-029-386-941; Sequence 941, Application US/10029386; Publication No. US20030194704A1
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US-10-027-632-188583
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
                                                           GENERAL INFORMATION:
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Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 188583
LENGTH: 507
                                                                                                                                                                                                                                                                                                 Query Match
Best Local
APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                                                                                         1 GGGTCTGCAGCGGATGGT 19
                                                                                                                                                                                                                                                                                17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                    GGGTCTGCAGCAGGGTGGT 36
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                                                                                                                                                                                                                                                                                                 83.2%;
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89.5%;
                                                                                                                                                                                                                                                                                 Score 15.8; D
Pred. No. 2.7e
0; Mismatches
                                                                                                                                                                                                                                                                                 0;
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APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO

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OTHER INFORMATION: MAP TO CHR22 166.0

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72

OTHER INFORMATION: NT HIT: gill418060, EVALUE 2.00e-50

OTHER INFORMATION: EST HUMAN HIT: BF884753.1, EVALUE 3.00e-28

OTHER INFORMATION: SWISSPROT HIT: P32927, EVALUE 3.00e-16
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
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Best Local Similarity 85..
Thes 17; Conservative
                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 159729
LENGTH: 868
TYPE: DNA
ORGANISM: Human
S-10-027-632-159729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 159729, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 941
LENGTH: 589
                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-027-632-159729/c
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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372
                                                                                          l Similarity
17; Conserv
                                            GGGTCTGCAGCGGGATGGT 19
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GGGTCTGCAGGGGGACGGT 354
                                                                                           Conservative
                                                                                                                 83.2%;
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89.5%;
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                                                                                                                 Score 15.8; DB 13; Length 868; Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 15.8; DB 13; Length 589; Pred. No. 2.6e+02;
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                                                                                           Mismatches
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RESULT 23 US-10-027-632-159729/c

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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,358

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09-09
PRIOR PILING DATE: 1999-09-09-09
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                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: PastSEQ for
SEQ ID NO 174763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 159729
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                     TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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NAME/KEY: misc_feature
LOCATION: (1)...(2940917)
                                                                                                                                              ENGTH: 2940917
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17; Conserv
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; OTHER INFORMATION: n = A,T,C US-10-027-632-174763
          APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                       Sequence 44678, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 174763
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Best Local
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 108827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1)...(2940917)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2940917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 89.1
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                                                                                                                                                                                                                                                                                                                                                                                                   299508
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                 GGGTATTCAGCGGGATGGT 299490
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CATION NUMBER: US 60/360,039
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Pred. No. 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15.8;
Pred. No. 83
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                                                                                                           IN PLANTS FOR PRODUCTION OF
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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44678
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: SYNECHOCOCCUS SP. WH 81
US-10-369-493-44678
APPLICANT: Kmiec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
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US-09-939-964-1/c
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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Best Local Similarity
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APPLICANT: Freiberg, Christoph
TITLE OF INVENTION; William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
FILE REFERENCE: CARPO068
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
CURRENT FILING DATE: 2001-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/214,808 PRIOR FILING DATE: 1999-06-22 NUMBER OF SEQ ID NOS: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
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94.1%;
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94.1%;
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Pred. No. 1.7e+02;
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Pred. No. 3.6e+02;
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US-10-209-787-1345
; Sequence 1345, Application US/10209787
; Publication No. US20030217377A1
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-818-875-1346
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; ORGANISM: Homo sapiens
US-09-818-875-1345
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SOFTWARE: Friedman macro Napro4
SEQ ID NO 1346
LENGTH: 121
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LENGTH: 121
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                                                         FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/10/209,787
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 09/818,875
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-03-03
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-03-03-03
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-10-30
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APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
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APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
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                    APPLICATION NUMBER: US 60/192,179 FILING DATE: 2000-03-27
APPLICATION NUMBER: US 60/208,538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pred. No.
:ive 0; Mismatc
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. 7.8e+02;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-209-787-1345
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PRIOR APPLICATION NUMBER: US 09/818,875
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
                Sequence 28, Application US/10429802
Publication No. US20030228285A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: WONG, KA YIN
APPLICANT: ZOU, YIYU
TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
FILE REFERENCE: UTSC:752US
CURRENT APPLICATION NUMBER: US/10/429,802
CURRENT FILING DATE: 2003-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Fri
SEQ ID NO 1346
                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1346, Application US/10209787 Publication No. US20030217377A1
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides FILE REFERENCE: Napro-4 CURRENT APPLICATION NUMBER: US/10/209,787 CURRENT FILING DATE: 2002-07-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/244,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
PRIOR APPLICATION NUMBER: 60/377,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gamper, Howard I APPLICANT: Rice, Michael C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Friedman macro Napro4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 121
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 78.9%; Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                          GGGTCTGCAGCGGGA 15
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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. 7.8e+02;
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; LENGTH: 340
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-429-802-28
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JS-09-016-869B-22
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NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 340
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TELEFAX: (617) 951-705
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,869B
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
                                                      ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: GPCI-P10-071

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 951-7739

TELEPAX: (617) 951-7050
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APPLICANT: Demetrick,
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ZIP: 02110
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 25-MAN
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FILING DATE: 14-SEP-1994
TOR ADDITIONATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/893,274 FILING DATE: 15-JUL-1994
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One International Place
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                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 08/248,812
25-MAY-1994
                                  7) 55
, 951-7050
NO: 22:
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100.0%; Pred. No. 6.9e+02;
htive 0; Mismatches 0;
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Best Local Similarity
Matches 15; Conserv
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                                                                      TELEFAX: (617) 951-7050 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
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                                                                                                     REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: GPCI-P10-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 951-7739
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-JAN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/016,869B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
TITLE OF INVENTION: Uses Related Thereto
                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE
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                                                                                                                                                                                FILING DATE: 17-DEC-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/893,274
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                          LENGTH: 404 base pairs
                                                                                                                                                                                                              APPLICATION NUMBER:
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US200
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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linear
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17-DEC-1992
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100.0%; Pred. No.
tive 0; Mismatc
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; NAME/KEY: CDS; LOCATION: 1..1146; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-09-908-671-1
В
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                                                                     Matches
                                                                                   Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: CARSON, DENNIS A.
NOBORI, TSUTOMU
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/908,671
FILING DATE: 18-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/227,800
FILING DATE: 14-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: HOWELLS, STACY L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: 07340/0230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
les 15; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TUMOR SUPPRESSOR GENE AND METHODS FOR DETECTION OF CANCER, MONITORING OF TUMOR PROGRESSION AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070
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GGGTCTGCAGCGGGA 539
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                                  GGGTCTGCAGCGGGA 15
                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                             LENGTH: 1146 base pairs
                                                                                                                                                                                                                                                                                                                                                                                      relefax: 619/678-5099
                                                                                                                                                                                                                           JIBRARY: 5'region of CDK4I (genomic)
                                                                     Conservative
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100.0%; Pre
                                                                                78.9%; Score 15; DB 13; 100.0%; Pred. No. 5.8e+02;
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Pred. No.
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                                                                                                   Length 1146;
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S
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US-09-993-525-11
                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                    US-10-156-761-7227/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-984-664-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 52
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hanna, M
                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                  Sequence 7227, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Production of Secreted Polypeptides FILE REFERENCE: GC618
CURRENT APPLICATION NUMBER: US/09/993,525
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: WO PCT/US99/31010
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Molecular Detection Systems Utilizing Reiterative Oligonucleotide TITLE OF INVENTION: Synthesis FILE REFERENCE: 2072.0010000 CURRENT APPLICATION NUMBER: US/09/984,664 CURRENT FILING DATE: 2001-10-30 NUMBER OF SEQ ID NOS: 17
                                                                                              APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Diaz-Torres, Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
ICANT: SAKAKİ, YOSHIYUKI
ICANT: HATTORI, MASAHIRA
E OF INVENTION: NOVEL POLYNUCLEOTIDES
REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2378
                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 78.9%; S
l Similarity 100.0%;
15; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGTCTGCAGCGGA 15
                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                    GGGTCTGCAGCGGGATGG 18
                                                                                                                                                                                                                                                                  GCGCCTGCAGCGGGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTCTGCAGCGGGA 2392
                                                              ISHIKAWA, JUN
HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09993525
No. US20030032093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09984664
                                                                                                                                                                                                                                                                                                                                     Conservative
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88.9%;
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k; Pred. No. 5e+
0; Mismatches
                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                    Score 14.8;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
5e+02;
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; NAME/KEY: misc_feature
; LOCATION: (33)..(33)
; OTHER INFORMATION: n can be any nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces avermitilis; FEATURE:
NAME/KEY: CDS; LOCATION: (1)...(219)
US-10-156-761-7227
                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 7227
LENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
SEQ ID NO 69
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/10339604 Publication No. US20030152982A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: Oligonuclectide Molecules for Use in Detection of Mycobacterium
TITLE OF INVENTION: Antibiotic Resistance
FILE REFERENCE: 1657.0010001
CURRENT APPLICATION NUMBER: US/10/339,604
CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US/99/722,319
PRIOR APPLICATION NUMBER: US 08/750,088
PRIOR APPLICATION NUMBER: US 08/750,088
PRIOR FILING DATE: 1996-12-06
PRIOR APPLICATION NUMBER: PCT/EP95/02230
PRIOR APPLICATION NUMBER: PCT/EP95/02230
PRIOR FILING DATE: 1995-06-09
PRIOR APPLICATION NUMBER: EP 94870093.5
PRIOR FILING DATE: 1994-06-09
NUMBER OF SEQ ID NOS: 73
NUMBER: Deterting variation 3 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTABLS, FRANCOIS
APPLICANT: MACHTELINCKX, LIEVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-339-604-69/c
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Probe
                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (8)..(8)
OTHER INFORMATION: n can be any nucleotide
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76
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGTCTGCAGCGGGATGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTCGGCAGCGGGCTGG
 GGGTCTGCGGCGTGATGG 59
                                    GGGTCTGCAGCGGGATGG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.9%;
nilarity 88.9%;
Conservative
                                                                           77.9%;
ilarity 88.9%;
Conservative
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                                                                         Score 14.8; DB 13;
Pred. No. 9e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14.8; DB 15; Pred. No. 9.1e+02; 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 219;
                                                                                                                     Length 228;
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; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701065580H1
US-09-878-574-12285
밁
                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 40
US-09-878-574-12285/c
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 12285
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: D....
                                                                   Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                       APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
TITLE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
                                                                                   Match 77.9%; Local Similarity 88.9%;
59
                               1 GGGTCTGCAGCGGGATGG 18
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GGGTCTGCATCGGGAAGG
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 42
                                                                  Score 14.8; DB 10
Pred. No. 8.8e+02
0; Mismatches
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                                                                                                    Length 276;
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Search completed: January 13, 2004, 21:03:11 Job time: 139.5 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       January 13, 2004, 15:53:18; Search time 36.5 Seconds (without alignments) 229.761 Million cell updates/sec
Sequence 1, Appli
Sequence 4370, Ap
Sequence 4, Appli
Sequence 7, Appli
Sequence 3819, Ap
Sequence 3775, Ap
Sequence 3775, Ap
Sequence 1, Appli
Sequence 2, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION:
US-07-960-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              00000000000000
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                      OPERATING SYSTEM: System Software 7.
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/960,389
FILING DATE: 07-JAN-1993
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: 554,745
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 18-JUL-1990
APPLICATION NUMBER: PCT/US 91/04846
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Blasdale, John H. C.
REGISTRATION NUMBER: 31,895
REFERENCE/DOCKET NUMBER: DX0143Q
TELEPHONE: (908) 298-2902
TELEPHONE: (908) 298-2902
                                                                                                                                                              TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3475 base pairs
TYPE: nucleotides
                                                                                               LENGTH: 3475 base pairs
TYPE: nucleotides
STRANDEDNESS: single
TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disc
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HAYASHIDA, Kasuhiro;
TITLE OF INVENTION: Human GM-CSF Receptor Component
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Kenilworth
STATE: New Jerse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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36941
      100.0%;
                                                                  DNA sequence encoding Human GM_CSF receptor
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US-09-120-131-3
US-09-120-131-3
US-08-311-731A-130
US-08-750-088A-69
US-09-147-935A-11
US-09-147-935A-17
US-09-147-935A-18
US-09-147-935A-22
US-09-147-935A-28
US-09-147-935A-28
US-09-147-935A-35
US-09-750-088A-35
US-09-750-088A-35
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      Score 19;
Pred. No.
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      DB 2.4;
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                    Length 3475;
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Sequence 3, Appli
Sequence 130, Appli
Sequence 11, Appl
Sequence 69, Appl
Sequence 5, Appli
Sequence 11, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 29, Appl
Sequence 35, Appl
Sequence 35, Appl
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Sequence 36, Appl
Sequence 37, Appl
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Issued Patents NA:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Result

Query Match Length

DВ

Description

SUMMARIES

19

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1 4403765
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4001
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US-07-960-389-1
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US-08-8486-047-3
US-08-9120-130-3

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Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Total number of

hits satisfying chosen parameters:

569978 seqs, 220691566 residues

Title: Perfect score:

US-09-719-737-9 19

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Run

on:

OM nucleic - nucleic search, using sw model

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen

Ltd

Sequence:

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 4216

LENGTH: 1455

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4370
LENGTH: 1350
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                                 US-09-341-587-4/c
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US-09-252-991A-4216
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US-09-252-991A-4370/c
                                                     RESULT 4
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
Sequence 4, Application US/09341587 Patent No. 6346606
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Best Local
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Best Local
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17; Conserv
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94.4%;
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Pred. No. 40;
0; Mismatches
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Pred. No. 40
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Sequence 7, Application US/09341587

Patent No. 6346606

GENERAL INFORMATION:
APPLICANT: Mollenhauer, Jan
TITLE OF INVENTION: Protein Containing an SR(
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-4
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US-09-341-587-7/c
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SEQ ID NO 3819
LENGTH: 480
TYPE: DNA
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Best Local Similarity
Matches 17; Conserv
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                                                  APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Best Local Similarity
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TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08-31
CURRENT FILING DATE: 1999-08-31
CARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Homo sapiens
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Pred. No. 4:
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Pred. No. 4
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3775
LENGTH: 897
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3819
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; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. F
                                                                                                                                                   APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3591
LENGTH: 1272
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
ORGANISM: Pseudomonas aeruginosa
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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Best Local
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ORGANISM: Pseudomonas aeruginosa
-09-252-991A-3775
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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les 16; Conserv
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                                                                                          Similarity
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GGTCTGCAACGGGATGG 695
                                    GGTCTGCAGCGGGATGG 18
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94.1%;
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                                                                     Score 15.4; DB 4; Length 1272; Pred. No. 1.2e+02; 0; Mismatches 1; Indels 0
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Pred. No. 1.
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Pred. No. 1.1e+02
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; TYPE: DNA; ORGANISM: Rhizobium US-09-214-808-1
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US-09-214-808-1/c
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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TITLE OF INVENTION: Plasmid
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                                                                                 Query Match
Best Local
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APPLICANT:
                                                                   Matches
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CURRENT APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 1999-06-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                              OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or {\bf g}
                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 536165
                                                                                                                                                                                                                                                     ENGTH: 4403765
 4102066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                 Similarity
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 GGGTGTGCAGCGGGATG
                                 GGGTCTGCAGCGGGATG
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Perret, Xavier Philippe
Broughton, William John
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                                                                   Conservative
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                                                                                 81.1%;
94.1%;
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94.1%;
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  4102082
                                                                  Score 15.4; D
Pred. No. 85;
0; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                              FOR STRAIN ANALYSIS IN MYCOBACTERIUM
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                                                                                                 Length 4403765;
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RESULT 11 US-09-103-840A-1 ; Sequence 1, Application US/09103840A

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RESULT 12
US-08-581-918A-27
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
-09-103-840A-1
                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION ATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: US 08/36,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
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APPLICANT: WHITE, OWE
APPLICANT: FRASER, CI
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ent No.
                                         APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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PPLICANT: Hannon, Gregory J.
TILE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TILE OF INVENTION: Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Foley, Hoag & Eliot
One Post Office Square
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MBER: US 08/227,371
14-APR-1994
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Pred. No. 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                 APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Serrano, Manuel APPLICANT: Hannon, Gregory J. TITLE OF INVENTION: Cell-Cycl TITLE OF INVENTION: Related T
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-NOV-1993 PRIOR APPLICATION DATA:
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: WORDPACE
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                                                    APPLICATION NUMBER:
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CANT: Beach, David H.
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15; Conserv
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One Post Office Square
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                TUMBER: US 08/154,915
18-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell-Cycle Regulatory Proteins, and Uses
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US 07/991,997
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hes 0;
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                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/497,214D
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NUMBER: US 08/248,812
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
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APPLICANT: Beach, David H.

APPLICANT: Demetrick, Doug

APPLICANT: Serrano, Manuel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tent No. 6331390
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LENGTH: 401 base pairs
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Cell-Cyc
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-346-147B-27
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REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
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CITY: Boston
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EDNESS: single
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One Post Office Square
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serrano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hannon, Gregory J.
VENTION: Cell-Cycle Regulatory Proteins, and Uses
                                                                             TUMBER: US 08/154,915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Douglas J.
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hes 0;
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Best Local S
                                                                                                                                                                                                                                                                 AFFILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/346,147
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                                                                                                                   FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 25-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US U8/370,-
APPLICATION NUMBER: US U8/370,-
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/306,511
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
                                APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 832-1299
                                                                                    FILING DATE: 14-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 401 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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15; Conservative 0;
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One Post Office Square
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                                                                                                     14-APR-1994
MBER: US 07/991,997
17-DEC-1992
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                                                                                                                        US 08/227,371
                                                                                                                                                                           US 08/248,812
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1.7e+02;
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RESULT 16
US-08-346-147B-26
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                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIOR APPLICATION NUMBER: US 08/227,371
APPLICATION NUMBER: US 08/227,371
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICANT: Beach, David H.

APPLICANT: Demetrick, Douglas J.

APPLICANT: Serrano, Manuel

APPLICANT: Hannon, Gregory J.

TITLE OF INVENTION: Cell-Cycle Regul

TITLE OF INVENTION: Related Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                      APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1299
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US ZIP: 02109
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                                        NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
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40, 6211334
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One Post Office Square
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RESULT 17
US-08-497-214D-26
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GENERAL INFUR....

APPLICANT: Beach, Davidan J.

APPLICANT: Demetrick, Douglas J.

APPLICANT: Serrano, Manuel

APPLICANT: Serrano, Manuel

APPLICANT: Hannon, Gregory J.

TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

TITLE OF INVENTION: Related Thereto

TITLE OF SEQUENCES: 47

TITLE OF SEQUENCES: 47
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
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LENGTH: 404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DO SOFTWARE: WORD DATA: CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
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APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
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                              TELECOMMUNICATION INFORMATION: (617) 832-1299
                                                                                                                         FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 1
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APPLICATION NUMBER:
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Local Similarity 100.0%;
les 15; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                      NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.05
                                                                                                                                                                                                          APPLICATION NUMBER: US 08/154,915 FILING DATE: 18-NOV-1993
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                  832-7000
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Pred. No.
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                                                                            FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-1093.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                  TELEPHONE: 202-962-481
TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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LENGTH: 404 base pairs
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APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
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ENGTH:
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1149 base pairs
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US-08-474-177-3
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Best Local Similarity
Matches 15; Conserv
                                                      APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
PILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
PILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thren Jeffrey L.
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
APPLICATION NUMBER-1995
--- nate: 17-Mar-1995
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
REFERENCE/TION INFORMATION:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                    INFO...
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100.0%; Pred. No.
tive 0; Mismatch
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Query Match
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Marches 15; Conserva
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                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,810
FILING DATE: 07-JUN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
ADDITION NUMBER: 18-MAR-1994
PRIOR APPLICATION DATA:
ADDITION DATA: 19-MAR-1994
PRIOR APPLICATION DATA: 19-MAR-1994
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AOLECULE TYPE:
HYPOTHETICAL: NO
"TI-SENSE: NO
"AL SOURCE:
HOMO sapiens
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                     APPLICATION NUMBER: FILING DATE: 18-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
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                                          MBER: US 08/215,086
18-MAR-1994
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US-08-480-810-3
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,73:
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APPLICANT: Kamb, Alexander
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NUMBER OF SEQUENCES:
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Local Similarity 100.0%; F
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1201 New York Avenue, Suite 1000
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Pred. No.
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US-08-508-735-3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: .IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848,251
FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-195
APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FFILING DATE: 01-JUN-1994
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Best Local Similarity

Matches 15; Conserv
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NAME/KEY:
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ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE
TITLE OF INVENTION: GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                       STREET: 1201 New CITY: Washington STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION:
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100.0%; Pred. No. 1.8e+02;
^ Mismatches 0;
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US-08-848-251-3
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US-08-486-047-3
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Patent No. 5994095
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Best Local S
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE TATA hase pair
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
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ORIGINAL SOURCE:
ORGANISM: Homo
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MEDIUM TYPE: Floppy disk
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NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24
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CORRESPONDENCE ADDRESS:
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CITY: Washington
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PRIOR APPLICATION DATA:
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1201 New York Avenue, Suite 1000
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RESULT 24
US-09-120-130-3
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NAME/KEY:
LOCATION:
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                                                                                                   TITLE OF INVENTION: MTS1 GENE NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
ZIP: 20005
COMPUTER READABLE FORM:
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APPLICATION NUMBER:
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                                              STREET: 1201 New CITY: Washington STATE: DC
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                                                                                                                                                                                                                                                                                                                                             Local
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REFERENCE/DOCKET NUMBER:
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FILING DATE: 17-MAR-1995
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                          COUNTRY:
                                                                        ADDRESSEE: Venable, Baetjer, Howard & Civiletti, STREET: 1201 New York Avenue, Suite 1000
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US-09-120-130-3
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RESULT 25
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 1149 base pair
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APPLICATION NUMBER: 1
FILING DATE: 18-MAR-
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LOCATION:
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CLASSIFICATION:
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COMPUTER: IB
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                                                                                                       Gaps
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; Sequence 3, Application US/09115252 ; Patent No. 6060301 ; GENERAL INFORMATION: APPLICANT: Kamb, Alexander TITLE OF INVENTION: MTS1 GENE ; NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:

US-09-115-252-3

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-09-115-252-3
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                                                                                                          Query Match
Best Local Similarity
Matches 15; Conserv
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PRIOR APPLICATION NUMBER: US 08/215,086
PTLING DATE: 18-MAR-1994
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
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CITY: Washington
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1026 GGGTCTGCAGCGGA 1040
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APPLICATION DATA:
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18-MAR-1994
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US-08-986-515-3
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Query Match
Best Local Similarity
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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PRIOR APPLICATION DATA:

US 08/227,369
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MEDIUM TYPE: Floppy
                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                  HYPOTHETICAL: NANTI-SENSE: NO ORIGINAL SOURCE:
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APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                 NAME/KEY:
LOCATION:
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CITY: Washington
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
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1017..1149
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18-MAR-1994
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   78.9%; Score 15; DB 3; Length 1149; 100.0%; Pred. No. 1.8e+02;
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Matches

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RESULT 27

09-120-128-3

GENERAL INFORMATION:

TITLE OF INVENTION: NUMBER OF SEQUENCES:

Kamb,

DDRESSEE:

Washington

COUNTRY: US ZIP: 20005

USA

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Sequence 3, Application US/09120128 Patent No. 6140473
                                                                                                                                                                                                      TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,047
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
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                                                  ORGANISM: Homo sapiens
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1201 New York Avenue, Suite 1000
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18-MAR-1994
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18-MAR-1994
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N: MTS2 GENE
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; LOCATION:
US-09-120-128-3
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US-09-120-129-3
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Best Local Similarity
Marches 15; Conserve
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Patent No. 6180776
                                                                       INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 08/486,047

FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
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                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 17-MAR-
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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CITY: Washington
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/120,129 FILING DATE: CLASSIFICATION:
                                                                                                                                        NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
LENGTH: 1149 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08 FILING DATE: 01-JUN-1994
                                                                                                        TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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1201 New York Avenue, Suite 1000
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867..1016
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100.0%; Pred. No.
tive 0; Mismatcl
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ORIGINAL SOURCE: HYPOTHETICAL:

NAME/KEY: LOCATION:

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NTI-SENSE:

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MOLECULE TYPE:

APPLICATION NUMBER: FILING DATE: 14-AP

APPLICATION NUMBER:

APPLICATION NUMBER: FILING DATE: 18-MA

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US-09-201-139-3
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Best Local Similarity
Matches 15; Conserv
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                                                                                                           TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO: 3:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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NAME/KEY:
LOCATION:
                                                                                                                                     REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION: 202-962-4848
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NAME/KEY:
                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/I
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANI: Jiang, Piny
APPLICANT: Jiang, Piny
Kamb, Alexander
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         MOLECULE TYPE:
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                                                                                                                                                                               NAME: Ihnen, Jeffrey REGISTRATION NUMBER:
                                       STRANDEDNESS:
TOPOLOGY: li
                                                     TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                ENGTH:
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                                                                              1149 base pairs
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                        DNA (genomic)
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RESULT 30
US-09-120-131-3
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Patent No. 6218146
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 18-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 01-JUN-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE: ORGANISM: Hom
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APPLICATION NUMBER: US 08/486,047
FILING DATE: 07-JUN-1995
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NAME/KEY:
                                                                                FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                APPLICATION NUMBER: US OF FILING DATE: 14-APR-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US OF APPLICATION NUMBER: US OF APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: 202-962-4810
                                                                                                                                                                                FILING DATE: 18-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                              NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                    REFERENCE/DOCKET NUMBER:
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INFORMATION FOR SEQ ID NO:

<u>..</u>

SEQUENCE CHARACTERISTICS:

ENGTH:

1149 base pairs

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US-09-120-131-3
                                         INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 36941 base pairs
TYPE: nucleic acid
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IS-08-311-731A-130
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                                                                                                                             FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No. 6583266
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
            OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                             DRRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLECULE TYPE:
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                                       STRANDEDNESS:
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                          TOPOLOGY:
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DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                    600 ATLANTIC AVENUE
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Best Local Similarity
Matches 15; Conserva
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US-08-750-088A-69/c
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CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: WO PCT/US99/31010
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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APPLICANT: DE
APPLICANT: PO
APPLICANT: MA
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TYPE: DNA
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OTHER INFORMATION: primer
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                                                       COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/750,088A
                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                STREET: 1100 Non
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                        STATE: D.C
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FILING DATE:
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1100 NEW YORK AVENUE,
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ROSSAU,
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 21-FEB-1997
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88.9%;
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No. 1.9e
0; Mismatches
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E, SUITE 600
                                                                                                                                                                                                                                                      DETECTION OF THE ANTIBIOTIC SPECTRUM OF MYCOBACTERIUM SPECIES
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2.2e+02
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Sequence 11, Application US/09147935A;
Patent No. 6242584;
GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF ROOB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
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; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-09-147-935A-5
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SOFTWARE:
SEQ ID NO 5
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Patent No. 6242584

GENERAL INFORMATION:

APPLICANT: KOOK, Yoon-Hoh

APPLICANT: KIM, Bum-Joon

TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpob GENE
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
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SOFTWARE: KOPATIN 1.0
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LENGTH: 228 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 77.9%;
Local Similarity 88.9%;
nes 16; Conservative
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REFERENCE/DOCKET NUMBER: 1657.0010000
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88.9%;
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Pred. No. 2.1e+02;
0; Mismatches 2;
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Pred. No. 2.1e+02;
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US-09-147-935A-18/c; Sequence 18, Application US/09147935A
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; ORGANISM: Mycobacterium genavense
US-09-147-935A-17
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GENERAL INFORMATION:
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LENGTH: 306
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LENGTH: 306
                                 Matches
                                                                  Query Match
                                                                                                                                                                        SEQ ID NO 18
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/147,935A CURRENT FILING DATE: 1999-03-19 PRIOR APPLICATION NUMBER: PCT/KR98/00228 PRIOR FILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                          APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
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                                                                                                                LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium gordonae
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RESULT 40
US-09-147-935A-29/c
; Sequence 29, Application US/09147935A
; Patent No. 6242584
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; SEQ ID NO 22
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-09-147-935A-22
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US-09-147-935A-28/c
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SEQ ID NO 28
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium nonchromogenicum
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Patent No. 6242584

GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
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Matches
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Best Local Similarity 88.9%;
Matches 16; Conservative
                  GENERAL INFORMATION: APPLICANT: KOOK, Y
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CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF xpoB GENE
FILE REFERENCE: 0136/0F425
   APPLICANT:
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KOOK, Yoon-Hol
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                                                                                                                                                                                    TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 29
LENGTH: 306
                                                                    Best Loc
Matches
                                                                                                     Query Match
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                               GGGTCTGCAGCGGGATGG 18
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Search completed: January 13, 2004, 17:58:34 Job time : 49.5 secs

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Query SUMMARIES

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ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX008655/c	RESULT 1
diseases and neoplastic cell proliferation Patent: WO 9966037-A 8 23-DEC-1999;	Antisense oligonucleotides for treating or preventing atopic	Renzi, P.		artificial sequences.	synthetic construct	synthetic construct		AX008655.1 GI:9996179	AX008655	Sequence 8 from Patent WO9966037.	AX008655 19 bp		
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Sequence 9 1
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                                     Renzi,P., Allam,M. and Allakhverdi,Z. Methods for increasing in vivo efficacy of inhibiting inflammation in mammals Patent: WO 03004511-A 8 16-JAN-2003; Topigen Pharmaceutiques Inc (CA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antisense oligonucleotides for treating or diseases and neoplastic cell proliferation Patent: WO 9966037-A 9 23-DEC-1999; RENZI PAOLO (CA); RECH EXPERTISES ET DEV ME Location/Qualifiers
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subunit of IL-3, IL-5 and GM-CSF human receptor"
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/mol_type="genomic DNA"
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/note="Sense oligonucleotide fo:
10 c 3 g 2 t
                          Location/Qualifiers
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organism="synthetic construct"
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Pred. No. 1.9e+02;
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Topigen Pharmaceutiques Inc (CA)
Location/Qualifiers
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Methods for increasing in vivo efficacy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-FEB-1991) Toshio Kitamura, Department of Molecular Biology, DNAX Research Institute of Molecular and Cellular Biolog 901 California Avenue, Palo Alto, CA 94304-1104, USA On May 16, 1994 this sequence version replaced gi:183367. Original source text: Human cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular cloning of a second subunit of the receptor for human granulocyte-macrophage colony-stimulating factor (GM-CSF): reconstitution of a high-affinity GM-CSF receptor Proc. Natl. Acad. Sci. U.S.A. 87 (24), 9655-9659 (1990)
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GM-CSF receptor; cytokine receptor; growth factor receptor;
lymphokine receptor.
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1 (bases 1 to 2996)
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mol_type="mRNA"
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TITLE
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                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 18, 1998 this sequence version replaced gi:2578146. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep CTA-833B7 is from the human BAC library described in U-J. Kim et al. (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
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                                                                                                                                                                                                                   assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. This sequence was generated from part of bacterial clone contigs human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                            IMPORTANT: This sequence is not the entire insert of clone CTA-833B7 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone CITF22-24E5 is at 100 in this so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Wellcome Trust Sanger Institute Center code: SC
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86574 bp DNA linear PRI 05-JUN-2003
Human DNA sequence from clone CTA-833B7 on chromosome 22q12.3-13.2
Contains the NCF4 gene for cytosolic neutrophil factor 4 (40kD),
the 5' part of the CSF2RB gene for granulocyte-macrophage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VECTOR: pBeloBAC11
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HTG; colony stimulating
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organism="Homo sapiens"
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                                                           ocation/Qualifiers
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complement(862. .903)
/note="MIR repeat: matches 212. .254 of consensus"
1072. .1084
/note="2.6 copies 5 mer GGAGA 26% conserved"
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1. .176
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                                /note="6.1 copies
conserved"
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complement(4478. .4555)
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| note="L2 repeat: matches 2636. .2819 of consensus"
| complement(6483. .6755)
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plement(4030. .4288)
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:e="2.5 (
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lement(1233. .1462)
le="L2 repeat: matches 2418. .2653 of consensus"
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3. .3277
3. .3277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                . .5370
.e="LIME1 repeat: matches 5523. .5604 of consensus"
blement(5371. .5676)

    . .4609
    .e="3.0 copies 6 mer CTGGGG 27% conserved"
    lement (4645. .5195)
    .e="LTR50 repeat: matches 4. .766 of consensus"

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lement(3872. .3956)
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                                                                                                                                                                                                                                                                                                                                                                                 /note="match: cDNAs: Em:AB002665 Em:X77094 Em:U59488 match: ESTs: Em:AA1177839 Em:AI007048 Em:AA465462 Em:AA465389 Em:AA485518 Em:AI381940 Em:AA744805 Em:AA975113 Em:AA969460 Em:AA948430 Em:AI435296 Em:AI299103 Em:AA648472 Em:AA702857 Em:AI088359 Em:D20144 Em:AA909156 Em:AA688071 Em:W95229 Em:AI439568" /evidence=not_experimental
                                                                                                                                                                                            /note="3.3 copies 3 mer GGA 20% conserved"
12443. 12453
/note="2.2 copies 5 mer GAGAC 22% conserved"
/note="2.2 copies 5 mer GAGAC 22% conserved"
join(12542. 12573,15415. 15499,16289. 16442,18762.
21785. .21912,23022. .23079,23697. .23795,27023. .271
277399. .27464,28998. .29193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="2.2 copies 5 mer TTTCA 22% conserved"
complement(11386. .11858)
/note="L2 repeat: matches 2722. .3312 of consensus"
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/note="2.0 (
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/note="MIR repeat: matches 184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 2. .191 of consensus" complement (7537. .7640)
                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2918. .3064 of consensus"
12358. .12367
                                                                                                                                                                                                                                                                                                                                                                  complement (11982.
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/note="2.6 copies 5 mer AGAGA 26% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(11913. .12573,15415. .15499,16289. .16442,18762. .18832,
21785. .21912,23022. .23079,23697. .23795,27023. .27153,
27399. .27464,28998. .29288)
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                                                                                                                                                                                          gene="NCF4"
                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="bK833B7.1 (neutrophil cytosolic factor 4
                                                                                                                                                                    note="match: proteins: Tr:060808 Tr:P97369"
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The="2.0 copies 8 mer TTGGGGGG 32% conserved"

03. .10313
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/mol_type="genomic DNA"
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a 3 c 9 g 5 t
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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2 (bases 1 to 2711)
Logsdon,N.J., Graham,A. and Scott,C.W.
Direct Submission
Submitted (19-MAR-1997) Target Discovery, Zeneca Pharmaceuticals, 1800 Concord Pike, Wilmington, DE 19850-5437, USA
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviic 1 (bases 1 to 2711)
Logsdon, N.J., Graham, A. and Scott, C.W. Guinea pig IL5 receptor beta chain
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1 (bases 1 to 783)
Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                          complete
U94688
                                                                                                                                                                                                                                                                                                                           Cavia porcellus interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                             Cavia porcellus
                                                                                                                                                                                                                                Cavia porcellus (domestic guinea pig)
                                                                                                                                                                                                                                                                      U94688.1 GI:3882357
                                                                                                                                                                                                                                                                                                                                               CPU94688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer A: None Primer B: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 6172521477
Fax: 6172580903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12466852
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                                                                                            Unpublished
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                                                                                                                                                                                                                                                                                                            cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/map="+ 16 40-713 30321911-30322586"
/clone_lib="CZECHII/Ei"
<1. .>783
202 c 199 g 201 t 1 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
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/strain="CZECHII/Ei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.6%;
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          550
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Pred. No. 7.5e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                              2711 bp
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                                                                                                                                                                                                                                                                                                                           receptor beta
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                                                                                                                                                                                                                                                                                                                           linear
a chain
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                                                                                                                                                                                            Euteleostomi;
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Fragment Name
AC120698_0
AC120698_1
AC120698_2
AC120698_3
Continuation (4 of 4) o
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ORIGIN
                                               ACCESSION
VERSION
KEYWORDS
                                                                                                                                    RESULT 15
AL954650/c
LOCUS
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                SOURCE
ORGANISM
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                                                                                                                  DEFINITION
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Best Local S
Matches 18
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                                                                                sequence.
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                                                  HTG.
             Homo sapiens
                                                                                                                  AL954650 8
Human DNA sequence from
 Eukaryota;
                                                                 AL954650.8
                                                                                                                                                                                                                                                                                                    91.6%;
Similarity 94.7%;
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                                                                                                                                                                                                                                                        GGGTCTGCAGCGGGATGGT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAC77520.1"
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IRSANHIQMAAPTLNVTKDGDTYSLRWVTEKMYYSHIENTFEIQYRTAGDRWENSKTE
TLKNAHNMPLPPLEPATTYLARVRVKPSPGGAYNGIWSEWSEQRWTTDWALPTWVLA
LVLVLVTLALLLALRFCGLYGYRLNRKWKEKIPNSKSHLFKNGSAGLRLPDSRMAFA
SRSAPSWGVMGGRFLEIEGVCPADSRDSEVSPLTTEDPTVVCDPPSEPHSTPAASDLT
QEQPPSVQPGPPVPQDQPGDQLATFDFNGPYLGPPHSHSLPDLAGQGPKPELPGSLE
YLCLPPGGRAQLVPLAQATGQAQPAPGECLSGPYLGPSPYLEDLAGQGPRPELPGSLA
QGPGDGPGDSPVILPTNSGGPEHPVVASGYVTTADLALTLSTEASSVSLAPPPDLCPG
LSDEAPAAPTPGKPRFEGYVELPASMGPLPKSFLGGFVPPAPSSPVLSPGTPQGDVSP
LSPAPEGLLVLQQVGDYCFLPGLGSGPLSPRSKPSSPVPCPEIMDIEQGFPVKKPPGQ
pMPQVPAIQFFKSLKQQDYLTLPPWEVSRPHEVC"

13 a 940 c 777 9 481 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Cavia porcellus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="IL5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="interleukin-5 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="IL5"
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                       100001
200001
300001
AC120698
                                                                                                                                                                                                                                                                                                                                                                                                                                         Begin
                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragments
                                                                    GI:28564367
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                                  (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                        Score 17.4; DB 2;
Pred. No. 4.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                          110000
210000
310000
367292
from base
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Pred. No. 6.4e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             End
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS AC120698 Accession AC120698
                                                                                                                   86257 bp DNA
a clone RP11-523M19
                                                                                                                                                                                                                                                                                                                                                            300001 (AC120698 Rattus
                                                                                                                                                                                                                                                                                                                         Length 67292;
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                                                                                                                      inear PRI chromosome
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                                                                                                                      26-FEB-2003
1, complete
                                                                                                                                                                                                                                                                                                                                                              norvegicus clone
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REFERENCE
AUTHORS
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AC120698 2/c
WPCOMMENT
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                                                  Continuation (3
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Best Local S
Matches 18
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  Query Match
                                                                                                                                                                                                   Sequence split into
                                                                          Fragment Name
AC120698 0
AC120698 1
AC120698 2
AC120698 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1

RP11-523M19 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                      59984
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 25, 2003 this sequence version replaced gi:28208053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-FEB-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. B-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martin, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                      GGGTCTGCAGCAGGATGGT 59966
                                                                                                                                                                                                                                                                                                                                                                                                   GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29602 a
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                                                    4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP11-523M19"
/clone_lib="RPCI-11.2"
13951 c 14808 g 27896 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/chromosome="1"
                                                    of AC120698
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                                                                                                    100001
                                                                                                                                                                         Begin
                                                                                                                                                                                                 fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .86257
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94.7%;
    91.6%;
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210000
310000
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Pred. No. 4.2e+02;
0; Mismatches 1;
                                                                                                                                                                               LOCUS
End
    Score 17.4;
                                                  from base 200001 (AC120698 Rattus norvegicus clone CH)
                                                                                                                                                                                                     AC120698 Accession
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 86257;
  Length 110000;
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VERSION
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AC117942/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.

E 1 (bases 1 to 142509)

RS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                               Submitted (05-SEP-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Sep 5, 2002 this sequence version replaced gi:20136917.
                                                                                                                                                                                                                                                                                                                       Submitted (11-APR-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC117942.2 GI:22725952
HTG; HTGS_PHASE2; HTGS_DRAFT.
Tetraodon_nigroviridis
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Tetraodon nigroviridis
                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                  Green, E.D
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Green, E.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                                                                                                                                                                                                                                    (bases 1 to 142509)
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Contact: nisc_zoo@nhgri.nih.go
                                                                                                                  Center: NIH Intramural Center code: NISC
                                                                                          Web site: http://www.nisc.nih.gov
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s clone
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                                                                                                                                         Sequencing Center
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GSTNB-27D21,
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WORKING DRAFT
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SEQUENCE, 4
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score. Sequencing vector: plasmid; n/a; 100% of reads Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 141403 bases at least Q40 Consensus quality: 141846 bases at least Q30

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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
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ORIGIN
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                        AC116440

AC116440

Tetraodon nigroviridis clone GSTNA-49N2, WORKING DRAFT SEQUENCE, 6 ordered pieces.

N AC116440

AC116440

AC116440.3 GI:24270692

HTG; HTGS_PHASE2; HTGS_DRAFT.

Tetraodon nigroviridis

EMATION RELEASES, Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontidea; Tetraodontidae; Tetraodonti
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1 19429: contig of 19429 bp in length
19430 19529: gap of unknown length
19530 107773: contig of 88244 bp in length
107774 107873: gap of unknown length
1107874 131292: contig of 23419 bp in length
131293 131392: gap of unknown length
131393 142509: contig of 11117 bp in length.
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This sequence will be replaced
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118928. .142509
/note="clone overlaps with GenBank Accession Number
AC116440 clone GSTNA-49N2 (center project name cvf)"
131393. .142509
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vector_side:r:
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="GSTNB-27D21"
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/note="Genoscope designation: COAB027D21"
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35682 c 34612 g
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Antonellis, A., Ayele, K.,
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94.7%;
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Pred. No. 3.
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Beckstrom-Sternberg, S.M.,
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 163158 bases at least Q30
Consensus quality: 16358 bases at least Q30
Insert size: 164032; sum-of-contigs
Quality coverage: 15.47x in Q20 bases; sum-of-contigs
* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 12551: contig of 12551 bp in length 67723 67822: gap of unknown length 67723 67822: gap of unknown length 87025 87124: gap of unknown length 87025 87124: gap of unknown length 92799: contig of 5675 bp in length 92799: contig of sof 5675 bp in length 92799: contig of unknown length
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Submitted (28-MAR-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Contact: nisc_zoo@nhgri.nih.gov
----- project Information
Center project name: cvf
Center clone name: 049N02
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Depublished

E (bases 1 to 177816)

E (bases 1 to 177816)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,

Anderson,S., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,

Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,

MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,

O'livor,T. Deferson,K., Phunkhang,P., Pierre,N., Pollara,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Ho
1 (bases 1 to 177816)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-429J17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177816 bp DNA linear PRI 30-SEP-2
Homo sapiens chromosome 8, clone RP11-429J17, complete sequence.
AC105219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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clone_end:SP6
vector_side:right"
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6 144425: gap of unknown length
6 164532: contig of 20107 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment"
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/note="Genoscope designation: COAAO49NO2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="GSTNA-49N2"
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94.7%;
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xref="taxon:99883"
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Pred. No. 3.9e+02;
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REFERENCE
AUTHORS
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Direct Submission

Blirect Submission

Submitted (09-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

22 4 (bases 1 to 177816)

23 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Weneus, L., Mihova, T., Mlenga, V., McCarthy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wunan, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wunan, D., Young, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wunan, D., Young, G., Zainoun, J., Volley, H., Wilson, B., Wilson, B.
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (30-SEP-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 30, 2002 this sequence version replaced gi:22759307. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                 Center project name:
/mol_type="genomic_DN
/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                organism="Homo sapiens"
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                         complement (30847. .30899)
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complement (30992. .31156)
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complement (36974. .36982)
/note="<a href="1.36982">1.36982</a>)
/complement (36992. .36998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2052...2362)
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complement(2382...2491)
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/clone_lib="RPCI-11 Human Male BAC"
complement(81. .161)
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complement(11974. .11978)
note="<30 qual SNGL region"
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complement(30523...30676)
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complement(27214..27447)
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39443. .39536
                                                                                                                                       complement (30847./rpt_family="1.1MC
                                                                                                                                                                                                                                      /rpt_family="L1MC5"
complement(29883 .30138)
/rpt_family="L1MC4a"
                                                                                                                                                                                                                                                                                                                                     complement (28420. .28556)
/rpt_family="L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(GGA)n"
complement(20089. .20093)
/note="<30 qual SNGL region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="<30 qual SNGL region"
20044. .20107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="single clone coverage"
complement(13117. .13132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="<30 qual single clone coverage"
3252. .13285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="(CCCG)n"
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[ement(13117. .13
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District

City (bases 1 to 200315)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Wyman, D., Ye, W.J., Young, G.,
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-125P19
Unpublished
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
Mus musculus
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42087. 4217
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41771. .41867
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94.7%; Pred. No. 3.8e+02;
tive 0; Mismatches 1
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3. .42770
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RS Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Roy,A., Schauer,S., Schupback,R., Scaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 36019: contig of 36019 bp in length 51874: contig of 100 bp 51874: gap of 100 bp 51975 75930: contig of 23956 bp in length 75931 76030: gap of 100 bp 104918 105017: gap of 100 bp 104918 105017: gap of 100 bp 104918 105017: gap of 100 bp 105018 178310: contig of 73293 bp in length 178411 200315: contig of 21905 bp in length 178410: gap of 100 bp 178410: gap of
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----- Project Information
Center project name: L18985
Center clone name: 125_P_19
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organism="Mus musculus"
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Angulano, D., Angulano, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Angulano, D., Baden, H., Baca, E., Baden, H., Baller, J., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Blawkin, D., Barnatead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Branstead, M., Calderon, E., Cavacos, I., Ceas, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Chen, Y., Duyalo, Y., Duyalo, Y., Palayan, Y., Palayan, Y., Chen, Y., Duyalo, Y., Palayan, Y., Chen, Y., Duyalo, Y., Chen, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246937 bp DNA linear Rattus norvegicus clone CH230-32J17, *** SEQUENCING ***, 6 unordered pieces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC111254.4 GI:30578635
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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a 46038 c 47231 g 53356
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105018. .178310
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clone_end:SP6
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178411. .200315_
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/clone_lib="RPCI-23 Female Mouse BAC"
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76031. .104917
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/db_xref="taxon:10090"
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IN PROGRESS
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Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pals, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Plopper, F., Rigger, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reeves, K., Regier, M.A., Reigh, R., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Waldron, L., Walker, B., Wang, J., Wallison, R., Wleczyk, R., Wei, X., White, F., White, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2003) Human Genome Sequencing Center; Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 13, 2003 this sequence version replaced gi:23269171. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Submitted (19-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246937)
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Milosavljevic,A., Miner,G., Minja,E., N
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                                                                                                             NOTE: Bstimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor Co
                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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COMMENT

TITLE
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AUTHORS

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TITLE JOURNAL

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RESULT 23
AX671174
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ORIGIN
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AX008662
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                                                                                                                                                                                                                                                                        Antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell proliferation Patent: WO 9966037-A 15 23-DEC-1999; RENZI PAOLO (CA); RECH EXPERTISES ET DEV MEDICAU (CA) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15
AX008662
 AX671174
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                                                                                                                    Conservative
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232662. .235507
/note="wgs_contig"
a 56226 c 53928 g
                                                                                                                                                                               /noTe="Antisense oligonucleotide inhibiting the common
subunit of IL-3, IL-5 and GM-CSF human receptor"
3 c 8 g 6 t
                                                                                                                                                                                                             /mol_type="yenom:32630"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                 construct
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237819: contig of 1047 bp in length
237919: gap of unknown length
240534: contig of 2615 bp in length
240634: gap of unknown length
242760: contig of 2126 bp in length
242860: gap of unknown length
242867: contig of 4077 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                              19 bp
from Patent WO9966037.
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236672: contig
236772: gap of
237819: contig
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                                                                                                                              89.5%;
                                                                                                                                                                                                                                     type="genomic DNA"
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Pred. No.
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Pred. No. 3
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                                                                                                                   Mismatches
   19
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hes 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Sequence is completely synthesized"
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/db_xref="taxon:32630"
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          2 (bases 1 to 10225)

Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, B., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, M.V.

Direct Submission
Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
                                                                                                                                                                                                                                                               Stover, C.K., Pham, X.-Q.T., Brwin, A.L., Mizoguchi, S.D., Walickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J. Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spewong, G.K.-S., Wu, Z. and Paulsen, I.T.

Complete genome sequence of Pseudomonas aeruginosa PA01, opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
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17; Conserv
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AE004803.1 GI:9950035
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Methods for increasing in vivo efficacy inhibiting inflammation in mammals
Patent: WO 03004511-A 22 16-JAN-2003;
Topigen Pharmaceutiques Inc (CA)
Location/Qualifiers
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Class 1: Function experimentally demonstrated in P. aeruginosa.
Class 2: Function of highly similar gene experimentally
Class 2: function of highly similar gene experimentally
demonstrated in another organism (and gene context consist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       updated, reviewed, Pseudomonas aeruginosa PAO1 genome annotation, from PseudoCAP (see http://www.pseudomonas.com for latest updates and links to alternate annotations). PseudoCAP is coordinated by Fiona S.L. Brinkman (Simon Fraser University, Canada) and Robert E.W. Hancock (University of British Columbia, Canada). We welcome submission through www.pseudomonas.com of any proposed changes.
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Direct Submission
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3: Function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene.
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/locus_tag="PA3858"
/note="synonym: aapJ"
/note="synonym: aapJ"
/complement (87. .112)
/locus_tag="PA3858"
/locus_tag="PA3858"
/locus_tag="PA3858"
/note="Protein name confidence: Class 3 (function proposed note="Protein name conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene); Subcellular localization: periplasmic; Subcellular localization confidence: Class 2"
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/note="Protein name confidence: Class 3 (function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene)"
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RNTSWTSSRDTALGIHFTGVTYFDGQGFLVNRKLGVSSARELKDATVCIQSGTTNELN
VADYFRAHGIRYKAVLDDSYEKSARALEAGQCDVLSSDQSQLYAQRLKLAKPEQYVVL
PEVISKEPLGPAVRQGDEAWFNIVRWTLYGLLNAEELGVTSSNVERQARDSRNPDVAR
LLGSEGDAGKDLQLPRDWVVQMVRQVGNYGEIFARNVGDGSPLKMPRGLNAQWNLGGL
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4584. .5777
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IVEIEPENVASDTVEGHVYAVAGSDKYKLLYNLVAQNNWERVMVFANRKDEVRRIEER
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/locus tag="PA3860"

/locus tag="PA3860"

/note="Protein name confidence: Class 3 (function proposed based on presence of conserved amino acid motif, structural feature or limited sequence similarity to an experimentally studied gene); Subcellular localization: Cytoplasmic; Subcellular localization confidence: Class 2"
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LRLDAIRRVLEEESRRIAEDIRVEVVADERHGQLAHLHVPALDERRQAALEELLGGYA
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5938. .6885
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SISTNAPRAHEVPAESLAAMDVYCDYRHTTPGSAGEMLIAAEQHGWSPEAIRGDLAEL
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previously reported genes of unknown function, or
similarity to any previously reported sequences)"
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PEDPDDYVHRIGRAGASGTSISFAGEDDAFALPPIEELLGRKITCEMPPAELLKP
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to functionally studied protein)"
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Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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Sequence 37 from Patent WO0100804.
AX066133
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94.4%;
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8.6e+02;
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AB020851
AB020851.1 GI:4996276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax:81-22-717-8047)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-DEC-1998) Akira Horii, Tohoku University School of Medicine, Department of Molecular Pathology; 2-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan [E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takeshita,H., Sato,M., Shiwaku,H.O., Semba,S., Sakurada,A., Hoshi,M., Hayashi,Y., Tagawa,Y., Ayabe,H. and Horii,A. Expression of the DMBT1 gene is frequently suppressed in human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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AB020817.1:89.136,AB020818.1:74..397,AB020819.1:84..113,
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APQSRPTPSPDTWPTSHASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDSW

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REFERENCE
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TITLE
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AB006797/c
                       FEATURES
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Molecular cloning and characterization of the oprQ gene coding for outer membrane protein OprE3 of Pseudomonas aeruginosa Microbiol. Immunol. 43 (3), 297-301 (1999)
                                                                                     Direct Submission
Submitted (22-AUG-1997) Hideto Tsujimoto, Kyoto Pharmaceutical
University, Laboratory of Microbiology; Misasagi Nakauchi-chou
Yamashina, Kyoto, Kyoto 607, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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99268523
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Tsujimoto, H.
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                                         (E-mail:htsujimo@mb.kyoto-phu.ac.jp, Tel:+81-75-595-4642,
Fax:+81-75-583-2230)
                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonadaceae; Pseudomonas.
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a 216 c 205
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-10_signal
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Sequence 109 from Patent EP1108790.
AX120193
AX120193.1 GI:14036908
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                                                                                                                                                                                                                                  Novel polynucleotides
Patent: EP 1108790-A 109 20-JUN-2001;
KYOWA HAKKO KOGYO CO., LTD. (JP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                   Similarity
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                                 GGTCTGCAGCGGGATGGT
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SYALDFAKYGVPGLTYRVAYVRGDNIKTAETSNGKEREIFNQVQYVVQSGPAKDLTLR
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60. .1437
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strain="PAO1"
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94.4%;
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                                                                 Score 16.4; D
Pred. No. 2.1e
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                                                                                4; DB 6;
2.le+03;
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                                                                                                                                                                                                                                                                                                                     Ochiai, K.,
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BD162310
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AUTHORS
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Best Local (
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PN JP 2002
PN JP 2002
PD 09-JUL-
PF 15-DEC-
PF SATOSHI
PI KAIKO OZAKI
PI C12N1/15,
PC C12N1/15,
PC C12N1/17
PC C12P19/
PC C12N13/566,
PC C12N15/
PC C12N15
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17; Conser
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KYOWA H
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                                                                                                                                                                                                                                                                                                                                                    AX066131
Sequence 35 from Patent
AX066131
                                                                                                                                                                                                    Corynebacterium glutamicum
Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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tolerance proteins Patent: WO 0100804-A 35 04-JAN-2001;
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Patent: JP 2002191370-A 109 09-JUL-2002;
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                                                            corynebacterium glutamicum genes encoding stress,
                                                                                        Pompejus,M., Kroeger,B.,
Lee,H.S. and Kim,H.J.
                                                                                                                                                                                                                                                                                                                           AX066131.1 GI:12543843
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C12P19/00,C12P19/34,C12P21/02,C12Q1/37,C12Q1/68,G01N33/53, PC
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15-DEC-2000 JP 2000405096
SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
KEIKO OCHIAI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAKKO KOGYO CO LTD
Corynebacterium glutamicum
JP 2002191370-A/109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
466 c 538 g 44
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                                                                                                                        Zelder, O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1824;
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                                                                                                                        Haberhauer, G.,
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Contact: niac mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens, Similar to RIKEN MGC:23427 IMAGE:4654320, mRNA, BC015649 BC015649.1 GI:15990514
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (04-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASF AKTIENGESELLSCHAFT (DE)
                                                                                                                                                                                                            cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Cor DNA Sequencing by: National Institutes of F Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2097)
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                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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ARSEQGEEGYEPSIRIRPVTKDRATFSLVDNGTGLTAQEARELLATVGRTSKRDEFGL
QREGRLGQFGIGLLSCFMVADEITMVSHAEGASAIRWTGHADGTFNLEILGDDATDVI
PVGTTVHLTPRPDERTLLTENSVVTIASNYGRYLPIPIVVQGEKNTTITTSPVFAKDT
DQQHRLYAGRERLGKTPFDVIDLTGPGIEGVAYVLPEAQAPHMSRRHSIYVNRMLVSD
GPSTVLPNWAFFVECEINSTDLEFTASREALMDDTAFAATREHIGECIKSWLINLAMT
KPHRVREFTAIHDLALRELCQSDADLAETMLGLLTLETSRGRISIGEITTLSITEDVS
LQLATTLDDFRQLNTIARPDTLIINGGYIHDSDLARLIPVHYPPLTVSTADLRESMDL
MELPPLQDIEKAKALDAQVTESLKDFQIKGATRVFEPADVPAVVIIDSKAQASRDRNE
TQSATTDRWADILATVDNTLSRQTANIPQDQGLSALCLNWNNSLVRKLASTDDTAVVS
RTVRLLYVQALLSSKRPLRVKERALLNDSLADLVSLSLSSDI"
99 a 502 c 562 g 484 t
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db_xref="GI:12543844"
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Pred. No. 2.1e+03;
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                                                                                                                                                                                             1 (bases 1 to 4690)
Semrau, J.D., Chistoserdov, A., Lebron, J., Costello, A., Davagni Kenna, E., Holmes, A.J., Finch, R., Murrell, J.C. and Lidstrom, M. Particulate methane monooxygenase genes in methanotrophs J. Bacteriol. 177 (11), 3071-3079 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methylococcus capsulatus particulate methane monoxygenase subunit (pmoCl), particulate methane monooxygenase 27 kDa subunit (pmoA), and particulate methane monooxygenase 45 kDa subunit precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 33 Row: i Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                           Methylococcus capsulatus
Bacteria; Proteobacteria; Gammap
Methylococcaceae; Methylococcus.
              Washington, Seattle, WA 98195
3 (bases 1 to 4690)
Stolyar, S.E. and Lidstrom, M.E
                                                             Submitted (14-MAR-1997) Chemical Engineering, University of Washington, Seattle, WA 98195, USA
                                                                                                        Lidstrom, M.E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Methylococcus capsulatus
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Submission
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1 740 c 658 g
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CGTGIRSSTSDPSRKPLDSRVLNAVKLYCQNFAPSFKESEMNVIAADMCTNARRVRKR
WLPKIKSMLPEGVEMYRTVMGSAAASVPLDPEFPPAAAAQVFEQRIYAERRGDAATIVA
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PRVSYYGVPSLATLIPGIQQMPYPQGERTSPGASSLPTTDSPTSYHNEEDDEEDDEAYD
TMVEEQYGQMYIKASGSYAVQEKPEPVPLESRSCVLIRRDLVALPASLISQIGYRCHP
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RAVLAASSLYFRDLFSGNSKSAFELPGSVPPACFQQILSFCYTGRLTMTASEQLVVMY
TAGFLQIQHIVERGTDLMFKVSSPHCDSQTAVIEDAGSEPQSPCNQLQPAAAAAAAPYV
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1. .2097
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/protein_id="AAH15649.1"
/db_xref="GI:15990515"
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clone_lib="NIH_MGC_41"
lab_host="DH10B-R"_
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mol_type="mRNA"
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lone="MGC:23427 IMAGE:4654320"
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Pred. No. 2.1e+03;
D; Mismatches 1;
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                                                                                          /gene="pmoB" 3443. .4585
                                                                                                                                                                                       VDAGRADELVSATDRKVAMGFLAATILIVVMAMSSANSKYPITIPLQAGTMRGMKPLE
LPAPTVSVKVEDATYRVPGRAMRMKLTITNHGNSPIRLGEFYTASVRFLDSDVYKDTT
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GSMSEFRNPVTTLTGQTVDLENYNEGNTYFWHAFWFAIGVAWIGYWSRRPIFIPRLLM
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3334. .3337
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/translation="MSAAQSAVRSHAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT
MGDWDFWSDWKDRRLWVTVTPIVLVTFPAAVQSYLWERYRLPWGATVCVLGLLLGEWI
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WPIIAPLHVPVENNGMLMSIADIQGYNYVRTGTPBYIRMVEKGTLRTFGKDVAPVSAF
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wsagldsfapefetywmnflyteivleivtasilwgylwktrdrnlaaltpreellrn
fthlvwlvayawaiywgasyfteodgtwhotivrdtdftpshiiefylsyfiyiitgf
aafiyaktrlpffakgislpylvlvvgpfmilpnvglnewghtfwfmbelfvaplhyg
                                                                                                                                                                  FFDATGNRQVVQIDAPLIPSFM"
                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
/product="particulate methane monooxygenase 45 kDa subunit
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(mol_type="genomic DNA"

(strain="Bath"
                                          product="particulate methane
                                                                   gene="pmoB"
                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAB49822.1"
/db_xref="GI:790832"
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db_xref="GI:790831"
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transl_table
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_xref="GI:1894818"
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Sequence 1 from Patent WO9830687.
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Poustka, A. and Mollenhauer, J.
PROTEIN CONTAINING AN SRCR DOMAIN
Patent: WO 9830687-A 1 16-JUL-1998;
DEUTSCHES KREBSFORSCH (DE); POUSTKA
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LVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWAMSAPGNARFQQS
GPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSH
ASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWA
TSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQS
QPTPSPDTWPTSRASTAGSESTLALRLVNGGDRCGRVEVLYQGSWGTVCDDYWDTND
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HEDAGVICSAAQSQSTPRPDTWLTTNLPALTVGSESSLALRLVNGGDRCRGRVEVLYR
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WSCPHKGWLTHNCGHHEDAGVICSATQINSTTTDWWHPTTTTTARPSSNCGGFLFYAS
GTFSSPYPAYYPNNAKCVWEIEVNSGYRINLGFSNLKLEAHHNCSPDYVBIPDGSLN
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TLDDVECSGTESTLWQCRNRGWFSHNCNHREDAGVICSGNHLSTPAPFLNITRPNTDY
SCGGFLSQPSGDFSSPFYPGNYPNNAKCVWDIEVQNNYRVTVIFRDVQLEGGCNYDYI
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TNLLCLPNHMQASVSRSYLQSLGFSASDLVISTWNGYYECRPQITPNLVIFTIPYSGC
GTFKQADNDTIDYSNFLTAAVSGGIIKRRTDTRITHVSTMYTATIPYSGC
GTFKQADNDTIDYSNFLTAAVSGGIIKRRTDTRITHVSTMYTATIPYSGC
GTFKQADNDTIDYSNFLTAAVSGGIIKRRTDTRITHYSGCRMLQNTWYDTMYIANDTMYIANDTHY
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                                                                                                                                                SVYLRCKMVVCRAYDPSSRCYRGCVLRSKRDVGSYQEKVDVVLGPIQLQTPPRREEEP
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NCQHSEDAGVICSAAHSWSTPSPDTLPTITLPASTVGSESSLALRLVNGGDRCQGRVE
VLYQGSWGTVCDDSWDTNDANVVCRQPGCGWAMSAPGNARFGQGSGPIVLDDVRCSGH
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/db_xref="GI:6739233"
/translation="MGISTVILEMCLLWGQVLSTGGWIPRTTDYASLIPSEVPLDQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="unidentified"
(mol_type="genomic DNA"
(db_xref="taxon:32644"
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Score 16.4; DB 6;
Pred. No. 1.8e+03;
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AR193170/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 5802)

E 1 (bases 1 to 5802)

E Mollenhauer, J. and Poustka, A.
Protein containing an SRCR domain
L Patent: JP 2001509667-A 1 24-JUL-2001;
DEUTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OFFENTLICHEN RECHTS

OS Homo sapiens (human)
PN JP 2001509667-A/1
PD 24-JUL-2001
PF 09-JAN-1998 JP 1998530469
PF 09-JAN-1997 DE 197 00 519.5, 18-JUL-1997 DE 197 30 997.6 PI
JAN MOLLENHAUER, ANNEMARIE POUSTKA
PC C12N15/12, C12N15/70, C12N1/21, C12Q1/68, C07K14/47, C07K16/18, PC
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Protein containing an SRCR domain.
BD064963
BD064963.1 GI:22610566
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1 (bases 1 to 5802)

Mollenhauer, J. and Poustka, A.

Mollenhauer, J. and Poustka, A.

Protein containing a scavenger receptor cysteine rich domain

Patent: US 6346606-A 4 12-PEB-2002;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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17; Conservative
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AR193170
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                                                                                                                           Protein containing an SRCR domain
Key Location/Qualifiers
CDS (107). (5461).
Location/Qualifiers
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1614 c 1576 g
                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
1614 c 1576 g 135
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94.4%;
  86.3%;
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KEYWORDS
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HSDMBT1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilgenbus, K.K., von Deimling, A. and Poustka, A. DMBT1, a new member of the SRCR superfamily, on ch 10q25.3-26.1 is deleted in malignant brain tumours Nat. Genet. 17 (1), 32-39 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-JUL-1997) Mollenhauer J., Molecular Genome Analysis, German Cancer Research Center, Im Neuenheimer Feld 280, Heidelberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mollenhauer,J., Wilgenbus,K.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alternative splicing; deleted in malignant brain tumors 1; DMBT gene; DMBT1/6kb.1 protein; tumor suppressor; tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mollenhauer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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sapiens mRNA for DMBT1 6
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                         /map="q25.3-q26.1"
/tissue_type="lung"
/dev_stage="fetal"
1. .5802
                                                                                                                                                                                                                                                                                                                          /gene="DMBT1"
/function="putative tumour suppressor"
/note="DMBT1 6kb transcript variant 1
deleted in malignant brain tumours
different DMBT1 transcripts can be gen
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ASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWA
TSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQS
                                                                                                                                                                                                                                                                                                                                                                                                           /gene="DMBT1"
107. .5464
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|mol_type="mRNA"
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chromosome="10"
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6 kb transcript variant
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1 (DMBT1 gene)
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MCU94337/c
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2 (bases 1 to 7080)

Stolyar,S., Peeples,T.L., Costello,A.M. and Li.
Direct Submission
Submitted (05-MAR-1997) Chemical Engineering,
Submitted (85-MAR-1997) WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylococcus capsulatus formylmethanofurane dehydrogenase subunit A-like protein gene, partial cds; and formylmethanofurane tetrahydromethanopterin formyltransferase-like protein, formylmethanofurane dehydrogenase-like protein, methane monooxygenase subunit C2 (pmoC2), methane monooxygenase subunit A2 (pmoA2), and methane monooxygenase subunit B2 (pmoB2) genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
17; Conserv
4 (bases 1 to 7080)
Stolyar,S., Franke,M.
Direct Submission
                                                                                                             Stolyar,S., Franke,M. and Lidstrom,M.E.
Expression of individual copies of Methylococcus capsulatus
particulate methane monooxygenase genes
J. Bacteriol. 183 (5), 1810-1812 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Stolyar, S., Costello, A.M., Peeples, T.L. and Lidstrom, M.E. Role of multiple gene copies in particulate methane monooxygenase activity in the methane-oxidizing bacterium Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                              capsulatus Bath
Microbiology 145 (Pt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylococcus capsulatus
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds.
U94337 AF273026
U94337.2 GI:13
                                                                                                                                                                                                                                                                                                                                                                                             Microbiology
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EVFDGPYRSSPLIARVCDGARGSFTSSSNFMSIRFISDHSITRRGFRAEYYSSPSNDS
TNLLCLPNHMQASVSRSYLQSLGFSASDLVISTWNGYYECRPQITPNLVIFTIPYSGC
GTFKQADNDTIDYSNFLTAAVSGGIIKRRTDLRIHVSCRMLQNTWVDTMYIANDTIHV
ANNTIQVEEVQYGNFDVNISFYTSSSFLYPVTSRPYYVDLNQDLYVQAEILHSDAVLT
LFVDTCVASPYSNDFTSLTYDLIRSGCVRDDTYGPYSSPSLRIARFRFAFHFLNRFP
SVYLRCKMVVCRAYDPSSRCYRGCVLRSKRDVGSYQEKVDVVLGPIQLQTPPRREEEP
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HEDAGVICSAAQSQSTPRPDTWLTTNLPALTVGSESSLALRLVNGGDRCRGRVEVLYR
GSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGNESYL
WSCPHKGWLTHNCGHHEDAGVICSATQINSTTTDWWHPTTTTTARPSSNCGGFLFYAS
GTFSSPSYPAYYPNNAKCVWEIEVNSGYRINLGFSNLKLEAHHNCSFDYVEIFDGSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="DMBT
182. .5461
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SYGLCAGRVEIYHGGTWGTVCDDSWTIQBAEVVCRQLGCGRAVSALGNAYFGSGSGPI
TLDDVECSGTESTLWQCRNRGWFSHNCNHREDAGVICSGNHLSTPAPFLNITRPNTDY
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1614 c 1576 g 1359 t
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                                                                                                                                                                                                                                                                                                     Peeples, T.L., Costello, A.M. and Lidstrom, M.E.
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94.4%;
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Pred. No. 1.8e+03;
                               and Lidstrom, M.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7080 bp
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On Apr 6, 2001 this sequence version replaced
Location/Qualifiers
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LINDYVAWTIRSAKAIGIKVVNPGGISAFKFNQRMLDLDEKHVYYSVTPRQILKSLAR
AVHELGVPHPLHVHGCNLGVPGNVETTLNTISGIEGLPMHLTHIQFHSYGVEGDRKFS
SGAARIAEAINANKNITIDVGQILFGQTVTASGDSMRQHANAGHAHPDKWVCMDIECD
AGCGVVPFKYRDKNFVNALQWCIGLETFLLIDDPWRVFLTTDHPNGAPFTTYPHLIRL
LMDKSFRNDMLATINPEAAALSTLGSIDREYSLYEIAIMTRAGAARLLGLTDRGHLGA
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/transI table=11
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/translation="MHETKQGEKRFTGAICRCSHRYNSMEVKMAATTIGGAAAAEAP
/translation="MHETKQGEKRFTGAICRCSHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTALSFTLKSPLRQRLDASPLVPDRLLGKSPKEIATLDLQYGNR RIAAADLFDIAGDDAESVRISGSPKLDFAGRGMTRGSLIIDGDAGAYVGMHMKGGRLC VSGSAGLYAACELKGGIVEICGNAGDLLGSALPGNKKGMSEGVVIVRGDAGDRVGDHM RRGSILIEGNAGMYLGARMTAGTIAVRGRIGACAGYAMKRGTLLVYGSPVSNRRHLQR LWFTYPRFPAFAPQRLSGLEYLLLGDSGVPVPGASTGRRPLGPRQG"
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GGGNFLILAESQPQALAACEAAIEAMRRIPNVIMPFPGGVVRSGSKVGSKYKTLPAST
NDAFCPTLKGQTRTELSPEIESVMEIVIDGLSDADIAKAMRAGIEAACGLGAANGIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="formylmethanofurane tetrahydromethanopterin
formyltransferase-like protein"
/protein_id="AAK30007.1"
/db_xref="GI:13559970"
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/translation="MIINGVHIDETSAEAFPMRATRVIVTAQNLKWAHHAAQAMTGFA
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                                                                                                      SLCEAVDEGLIAK"
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/transI_table=11
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/protein_id="AAK30006.1"
/db_xref="GI:13559969"
                                                                        4699.
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mol_type="genomic_DNA"
strain="Bath"
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                                                                                                                                                                                                                                                                                                                           Mollenhauer,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSA243224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DMBT1/8kb.1).
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Submitted (18-JUN-1999) Mollenhauer J., Molecular Genome Analysis, Deutsches Krebsforschungszentrum, Im Neuenheimer Feld 280, 69120
                                                                                                                                                                                                                                                                                                                                                                         Mollenhauer, J., Holmskov, U., Wiemann, S., Krebs, I., Herbertz, S., Madsen, J., Kioschis, P., Coy, J.F. and Poustka, A.

The genomic structure of the DMBT1 gene: evidence for a region with susceptibility to genomic instability
susceptibility to genomic instability
Oncogene 18 (46), 6233-6240 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DMBT1 gene; DMBT1/8kb.1 protein.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                Heidelberg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ243224.1 GI:6624921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCTGCAGCGGGATGGT
                                                                                                                                                                                                                                                                                         (bases 1 to 7656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43224 7656 bp mRNA linear PRI 27-
sapiens mRNA for DMBT1 protein 8kb transcript variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYPEDLLAEDGLSVSDNSPLAPGETRTVDVTASDAAWEVYRLSDIIYDPDSRFAGLLF
FFDATGNRQVVQIDAPLIPSFM"
1 2138 c 2220 g 1381 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTIHWYDLSWSKEKVKINETVEIKGKFHVFEGWPETVDEPDVAFLNVGMPGPVFIRKE
SYIGGQLVPRSVRLEIGKTYDFRVVLKARRPGDWHVHTMMVVQGGGPIIGPGKWITVE
GSMSEFRNPVTTLTGQTVDLENYNEGNTYFWHAFWFAIGVAWIGYWSRRPIFIPRLLM
VDAGRADELVSATDRKVAMGFLAATILIVVMAMSSANSKYPITIPLQAGTMRGMKPLE
LPAPTVSVKVEDATYRVPGRAMRMKLTITNHGNSPIRLGEFYTASVRFLDSDVYKDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSAAQSAVRSHAEAVQVSRTIDWMALFVVFFVIVGSYHIHAMLT MGDWDFWSDWKDRRLWVTVTPIVLVTPPAAVQSYLWERYRLPWGATVCVLGLLLGEWI NRYFNFWGWTYFPINFVPPASLVPGAIILDTVLMLSGSYLFTAIVGAMGWGLIFYPGN WPIIAPLHVPVBYNGMLMSIADIQGYNYVRTGTPEYIRMVEKGTLRTFGKDVAPVSAFFSAFMSILIYFMWHFIGRWPSNERFLQST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/db_xref="GI:1913912"
organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="methane monooxygenase subunit B2"
/protein_id="AAB51066.1"
/db_xref="GI:1913913"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MKTIKDRIAKWSAIGLLSAVAATAFYAPSASAHGEKSQAAFMRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="PmoB2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.4%;
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.6793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 16.4; DB 1;
Pred. No. 1.8e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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BASE COUNT
ORIGIN
Query Match 86.3
Best Local Similarity 94.4
Matches 17; Conservative
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CGWAMSAPGNAQFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLTHNCGHSEDAGVICS
APLSRPTPSPDTWPTSHASTAGPESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDSW
DTSDANVVCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGYESYLWSCPHNGWLSH
NCQHSEDAGVICSDTLPTITLPASTVGSESSLALRLVNGGDRCQGRVEVLYRGSWGTV
CDDSWDTNDANVVCRQLGCGWAMLAPGNARFGQGSGPIVLDDVRCSGNESYLWSCPHN
GWLSHNCGHSEDAGVICSGPESSLALGLVNGGDRCQGRVEVLYRGSWGTVCDDSWDTN
                                                                                                                                                                                                                                                                                                                                 RGSFTSSSNFMSIRFISDHSITRRGFRAEYYSSPSNDSTNLLCLPNHMQASVSRSYLQ
SLGFSASDLVISTWNGYYECRPQITPNLVIFTIPYSGCGTFKQADNDTIDYSNFLTAA
VSGGIIKRRTDLRIHVSCRMLQNTWVDTMYIANDTIHVANNTIQVEEVQYGNFDVNIS
FYTSSSFLYPVTSRPYYVDLNQDLYVQAEILHSDAVLTLFVDTCVASPYSNDFTSLTY
DLIRSGCVRDDTYGPYSSPSLRIARFRFRAFHFLNRPPSVYLRCKMVVCRAYDPSSRC
YRGCVLRSKRDVGSYQEKVDVVLGPIQLQTPPRREEEPR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTVCDDYWDTNDANVVCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESYLWSC
PHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSHASTAGSESSLALRLVNGGDR
CQGRVEVLYRGSWGTVCDDYWDTNDANVVCRQLGCGWATSAPGSARFGQGSGPIALDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHSEDAGVICSASQSR
PTPSPDTWPTSHASTAGSESSLALRLVNGGDRCQGRVEVLYRGSWGTVCDDYWDTNDA
NVVCRQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPHDGWLSHNCGHH
EDAGVICSASQSQPTPSPDTWPTSHASTAGSESSLALRLVNGGDRCQGRVEVLYRGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGDRCQGRVEVLYRGSWGTVCDDSWDTSDANVVCRRLGCGWATSAPGNARFGQGSGPI
VLDDVRCSGYESYLWSCPHNGWLSHNCQHSEDAGVICSAAHSWSTPSPDTLPTITLPA
STVGSESSLALRLVNGGDRCQGRVEVLYQGSWGTVCDDSWDTNDANVVCRQLGCGWAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DANVVCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESYLWSCPNNGWLSHNCG
HHEDAGVICSAAQSRSTPRPDTLSTITLPPSTVGSESSLTLRLVNGSDRCQGRVEVLY
RGSWGTVCDDSWDTNDANVVCRQLGCGWATSAPGNARFGQGSGPIVLDDVRCSGHESY
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RLVNGDGRCQGRVEILYRGSWGTVCDDSWDTNDANVVCRQLGCGWAMSAPGNAWFGQG
SGPIALDDVRCSGHESYLWSCPHNGWLSHNCGHGEDAGVICSAAQPQSTLRPESWPVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRMTIHFRSDISFQNTGFLAWYNSFPSDATLRLVNLNSSYGLCAGRVEIYHGGTWGTVCDDSWTIQEAEVVCRQLGCGRAVSALGNAYFGSGSGPITLDDVECSGTESTLWQCRNRGWFSHNCNHREDAGVICSGNHLSTPAPFLNITRPNTDYSCGGFLSQPSGDFSSPFYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RQLGCGWAMSAPGNARFGQGSGPIVLDDVRCSGNESYLWSCPHKGWLTHNCGHHEDAG
VICSATQINSTTTDWWHPTTTTTARPSSNCGGFLFYASGTFSSPSYPAYYPNNAKCVW
EIEVNSGYRINLGFSNLKLEAHHNCSFDYVEIFDGSLNSSLLLGKICNDTRQIFTSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSASQSQPTPSPDTWPTSRASTAGSE
STLALRLVNGGDRCRGRVEVLYQGSWGTVCDDYWDTNDANVVCRQLGCGWAMSAPGNA
QFGQGSGPIVLDDVRCSGHESYLWSCPHNGWLSHNCGHHEDAGVICSAAQSQSTPRPD
TWLTTNLPALTVGSESSLALRLVNGGDRCRGRVEVLYRGSWGTVCDDSWDTNDANVVC
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/db_xref="SPTREMBL:Q9UGM2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed in human adult lung"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="putative tumour suppressor, role in immune system and differentiation" /note="8kb protein, variant 1 alternative splice form of the DMBT1 gene that is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="10q25.3-q26.1"
/tissue_type="lung"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NY PNNAKCVWD I EVQNNYRVTV I FRDVQLEGGCNYDY I EVFDGPYRSSPL I ARVCDGA
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                                                                                                                                                                                     /product="DMBT1/8kb.1 protein"
2126 c 2166 g 1760 t
                                                                                                                                                                                                                                                               /gene="DMBT1"
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                                         86.3%; Score 16.4; DB 9; Length 7656; 94.4%; Pred. No. 1.8e+03;
0;
        Mismatches
        1; Indels
        0
        Gaps
        0;
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1 GGGTCTGCAGCGGGATGG 18

Db 7289 GGGTCTGCAGCTGGATGG 7272

Search completed: January 13, 2004, 17:57:04 Job time : 748 secs

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Result
No.
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Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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2:
                                                                                                                                                                                                                                                                                                                  score greater than and is derived by a
                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                      Score
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seq length: 2000000000
 19
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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                                                                                                                                                                                                      Query
Match
                                                                                                                                                                                                                                                                                                                is the number of results predicted by chance to have a ater than or equal to the score of the result being pririved by analysis of the total score distribution.
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Gapop 10.0 , Gapext 1.0
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19
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1000.0
1000.0
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1000.0
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ABX12699
ABX12700
ABX12700
AAS70201
AAD51325
ABX63546
AAQ21453
                                                                                                                                                           AAZ56193
                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5105512
                                                                                      Oligonucleotide 10
Human IL-3/IL-5/GM
Human IL-3/IL-5/GM
Human IL-3/IL-5/GM
                                                                                                                                                                                                      Description
                    DNA encoding novel Human receptor cDN Human cDNA #546 di
 Sequence
                                                                                                                                                                                                                                                                                                                                        printed,
 encoding
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DNA encoding novel	AAA44554 AAS70202	23	305 624	83.2 83.2	15.8 15.8	4 4 5 4
Drosophila melanog	ABL07534	23	10131	84.2	16	43
	ABL07535	23	7217	•	16	42
Human IL-3/IL-5/GM	ABX12691	25	19	84.2	16	41
Oligonucleotide 11	AAZ56196	21	19	•	_	40
C)	AAH64966	22	349980	86.3	σ	39 9
Human SC3 DNA. Ho	AAV49655	19	28720	86.3	σ.	96
Propionibacterium	AAS59568	23	21719	86.3		37
DNA encoding human	AAS33413	22	8047	86.3		36
DNA encoding human	AAS33414	22	8045	86.3		35
Human SRCR protein	AAV49652	19	5802	86.3		34
Drosophila melanog	ABL06358	23	3309	86.3	16.4	33
C. glutamicum SRT	AAF71001	22	1947	86.3		32
C glutamicum codin	AAH65074	22	1824	86.3		31
Human secreted pro	AAC79967	21	1537	86.3		30
capsulatus g	ABQ90381	24	1443	86.3	<u>ه</u>	29
M. capsulatus gene	ABQ90060	24	1320	86.3	σ	28
	ABL06359	23	1197	86.3	σ	27
Drosophila melanog	AAA94826		1194	86.3		26
Drosophila odorant	AAA72267	N	1095	86.3	σ	25
DNA encoding novel	AAS83466	N	825	86.3	ð	24
DNA encoding novel	AAS67706	N	825	86.3	g	23
Human immune/haema	AAK84430	N	536	86.3	S	22
Human immune/haema	AAK84431	N	535	86.3	ð	21
C. glutamicum SRT	AAF71002	N	436	86.3	σ	20
Human immune/haema	AAK63218	N	256	86.3	16.4	19
Human IL-3/IL-5/GM	ABX12702		19	•	17	18
Human IL-3/IL-5/GM	ABX12701	N	19	•	17	17
Human IL-3/IL-5/GM	ABX12694	N	19	•	17	16
Oligonucleotide 10	AAZ56199	N	19	89.5		15
Human IL-3/IL-5/GM	ABX12690	25	19	94.7	18	14
Human IL-3/IL-5/GM	ABX12689	25	19	94.7		13
Oligonucleotide 10	AAZ56195	21	19	94.7		12
Oligonucleotide 10	AAZ56194	21	L	94		11
Human cDNA differe	356	24	7	100.0	19	10
Human receptor gen	AAD51326	25	21968	100.0	19	9

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ALIGNMENTS

AAZ56193;

AAZ56193 standard; DNA; 19 BP

a a

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RESULT 1
AAZ56193
ID AAZ5
XX
AC AAZ5
XX
DT 28-M
XX
DE Olig
XX
Inte
KW Inte
KW Gran
XX
FON WO99
XX
WO99
XX
TO-J
XX
PF 17-J
XX
PF 17-J
XX
PF 17-J
XX
PR 17-J
XX
PI Renz
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XX
PI Renz
XX
XX
PI Renz
XX
XX
                                                                                                                                                                                                                                    Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide; asthma; allergy; cancer; receptor expression inhibitor; cytokine; inflammation; hypereosinophilia; eosinophil proliferation; granulocyte macrophage colony stimulating factor; GM-CSF; ss.
                                                                                                                                                                                                                                                                                                              Oligonucleotide 107A for IL-3/IL-5/GM-CSF receptor expression inhibition.
             WPI; 2000-097743/08.
                                          Renzi P;
                                                                                                17-JUN-1998;
                                                                                                                                                       23-DEC-1999.
                                                                                                                                                                                  WO9966037-A2
                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                         28-MAR-2000 (first entry)
                                                                                                                          17-JUN-1999;
                                                                   (REEX-)
                                                                   RECH
                                                                    EXPERTISES & DEV MEDICAUX PARENZ
                                                                                               98CA-2235420
                                                                                                                           99WO-CA00572
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→ CONTROL OF CONT
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy; DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease; urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hypereosinophilia; cardiant; ophthalmological; cytostatic; antigense; neoplastic call proliferation; antisense; IL-3; IL-5; atopic disease; neoplastic disease; neo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5) receptor and the granulocyte macrophage colony stimulating factor (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5 and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines involved in eosinophil proliferation and survival, they are increased in asthma and atopic diseases, and are also involved in the indefinite proliferation of certain neoplastic diseases. The invention relates to antisense oligonucleotides directed against a nucleic acid sequence encoding either a chemokine receptor (CCR3), a common subunit of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common subunit of IL-3, IL-5 and GM-CSF receptors. The antisense oligonucleotides can be used in the treatment or prevention of asthma, allergy, hypereosinophilia, general inflammation or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABX12688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is an subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-2002; 2002WO-CA01046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2003
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                                                                                                         WPI; 2003-247944/24
                                                                                                                                                                                                       Renzi P,
                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-2001; 2001US-303071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003004511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interleukin-3 receptor; interleukin-5
                                                                                                                                                                                                                                                                                                            (TOPI-) TOPIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                                                       Allam M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antisense oligonucleotide directed against the common beta the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                            PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72pp; English
                                                                                                                                                                                                       Allakhverdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antisense; I
; GM-CSF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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FFFXXXXOOOOOOOOOOOOOOOOOOOOOOO
                                                                                      The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleotide acid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, curinary system diseases, rheumatological diseases, urinary system diseases, cancers. The respiratory system diseases, urinary system diseases, cancers. The respiratory system diseases is a sickness associated with can inflammation of the lungs, the airways and/or the nose. The respiratory distress syndrome, cystic fibrosis, chronic obstructive clung diseases. Chronic bronchitis, esinusitis and hypereosinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. Chronic chasiles are more stable in the body, more adenosine. Abx12681-Abx12698 represent antisense oligonucleotides of for treating or reventing atomic diseases and neonlastic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one nucleotide substitute -
                                                                     for treating or preventing atopic diseases and neoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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RESULT 3
ABX12699/c
                                                                                                                                                  Matches
                                                                                                                                                             Query Match
Best Local 9
10-MAY-2003
                                             ABX12699 standard; DNA; 19
                                                                                                                                                   19;
                                                                                                                             1 GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                               Similarity
                                                                                                     GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                  Conservative
(first entry)
                                                                                                                                                              100.0%; Score 19; DB 25; 100.0%; Pred. No. 10;
                                                                                                                                                   <u>.</u>
                                                                                                                                                    Mismatches
                                                                                                                                                    0
                                                                                                                                                                         Length 19;
                                                                                                                                                     Indels
                                                                                                                                                     0
                                                                                                                                                      Gaps
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밁 S

Sequence 19 BP; 2

A;

3 C; 10 G; 4 T; 0 other;

0

urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hypereosinophilia; cardiant; ophthalmological; cytostatic; antiasthmatic; antiallergic; antinflammatory; immunosuppressive; atopic disease; neoplastic cell proliferation; IL-3; IL-5; Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy; DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease; interleukin-3 receptor; interleukin-5 immunosuppressive;
IL-3; IL-5;
; GM-CSF; ss.

Human IL-3/IL-5/GM-CSF receptor DNA, sense oligonucleotide 107S.

Homo sapiens

WO2003004511-A2

16-JAN-2003

08-JUL-2002; 2002WO-CA01046.

06-JUL-2001; 2001US-303071P

Increasing in vivo efficacy

of a nucleic

acid molecule that

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(TOPI-) TOPIGEN PHARM INC.

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The present invention relates to a method for increasing the in vivo cc efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2'6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide cc substitutions are useful for increasing in vivo efficacy of a nucleot cc acid molecule that is administered to a mammal. The DAP-modified cligonucleotides are useful in antisense therapy for treating and/or cc preventing pulmonary/respiratory diseases, neurological diseases, cutinary system diseases, cutinary system diseases, cutinary system diseases, cancers. The respiratory system diseases, general inflammation and cc respiratory system disease is a sickness associated with cc respiratory system disease is selected from pulmonary fibrosis, adult respiratory distress syndrome, cystic fibrosis, chronic obstructive cling disease, chronic bronchitis, esinusitis and hypereosinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. CC DAP-modified oligonucleotides are more stable in the body, more considered from present sequence represents a sense oligonucleotides. The present sequence represents a sense oligonucleotides of adenosine. The present sequence represents a sense oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                       DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease; urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hypereosinophilia; cardiant; ophthalmological; cytostatic; antiallergic; antiallergic; antiniflammatory; immunosuppressive; atopic disease; neoplastic cell proliferation; antisense; IL-3; IL-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one
                                                                                                                                                                                                                                                                                                                             Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide 107A.
                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX12700 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19 BP; 4 A; 10 C; 3 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Examples; Page 18; 63pp; English
                                                             interleukin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                   inflammation; 2'6'-diaminopurine; DAP; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTCTGCAGCGGGATGGT 1
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                             receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
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                                                             receptor; GM-CSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
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RESULT 5
AAS70201/c
ID AAS702
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AC AAS702
XX
DT 13-FEB
XX
DE DNA en
XX
Human;
KW Homo s
XX
OS Homo s
XX
PN WO2001
XX
PD 11-OCT
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                                                                                                                                                                                                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleotic acid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, can inflammation of the lungs, the airways and/or the nose. The respiratory system disease is a sickness associated with crespiratory distress syndrome, cystic fibrosis, chronic obstructive cung disease, chronic bronchitis, eosinophilic bronchitis, asthma, callergy, allergic rhinitis, sinusitis and hypereosinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. Cadenosine. The present sequence represents an antisense oligonucleotide cadenosine. The present sequence represents an antisense oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one
                                                                                                                                                                                                         13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Renzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-2002; 2002WO-CA01046
                                                                                                                                                                  DNA encoding novel human diagnostic protein #6005
                                                                                                                                                                                                                                            AAS70201;
                                                                                                                                                                                                                                                                               AAS70201 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examples; Page 18; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-247944/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUL-2001; 2001US-303071P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003004511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                                            1 GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                          GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Allam M, Allakhverdi Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 2 A; 3 C; 10 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ехатріев
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 19;
100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the present
                                                                                                                                                                                                                                                                                619
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 25;
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11-OCT-2001

WO200175067-A2

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RESULT 6
AAD51325/c
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CC specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                               5'UTR
                                                                                                                 Homo sapiens.
                                                                                                                                                                                  Human receptor cDNA.
                                                                                                                                                                                                                                                     AAD51325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                Human; receptor; leukaemia;
                                                                                                                                                                                                                    16-APR-2003
                                                                                                                                                                                                                                                                                    AAD51325 standard; cDNA; 3394 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 6005; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity
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                                                                                                                                                                                                                                                                                                                                                                     336
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)B; ABG06014.
                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       619
                                                                                                                                                                                                                                                                                                                                                                     GGGTCTGCAGCGGGATGGT 318
                                                                                                                                                                                                                                                                                                                                                                                                      GGGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 19; DB llarity 100.0%; Pred. No. 12; Conservative 0; Mismatches
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2000US-0649167.
                                                                                                                                                                                                                  (first entry)
                             /*tag= a
189..2273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 A; 203 C; 182 G; 113 T; 0 other;
                                                                                 ocation/Qualifiers
product= "Human receptor"
                                                                  ..188
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                                                                                                                                    cancer; gene therapy; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
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RESULT 7
ABX63546/c
ID ABX635
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AC Cardia
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AC CARD
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel human receptor proteins and nucleic acid molecules encoding such proteins. The invention is useful for preparing a composition for treating a disease or condition mediated by a human receptor protein e.g. leukaemia or cancer. The invention is also useful in gene therapy. The present sequence is human receptor cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene; 88; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gong
                                                                                                                                                                 28-JUL-2000;
08-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA #546 differentially expressed in activated vascular tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX63546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3394 BP; 713 A; 1011 C; 927 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 1A; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e.g., leukemia or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human receptor proteins, useful for preparing a composition for treating a disease or condition mediated by a human receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-129304/12.
P-PSDB; AAE33203.
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                                                                                                                                                                                                                                               08-JAN-2002; 2002US-0044090.
                                                                                                                                                                                                                                                                                                          26-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ischaemia-reperfusion injury; stroke;
                                                                                                            (BAND/) BANDMAN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'ŦJ
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Similarity 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGTCTGCAGCGGATGGT 267
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                                                                                                                                                               2000US-222469P.
2001US-260483P.
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WPI, 2003-110597/10

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RESULT 8
AAQ21453/c
ID AAQ21453;
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AC AAQ21453;
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DT 17-MAY-19;
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DE Sequence of the colony strong stron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cc used in gene therapy. The cDNAs of the invention may be used in a cc high-throughput methods for detecting differential expression of one or more cDNAs in a sample, or screening several molecules or compounds to identify a molecule or compound that specifically binds a cDNA of the cinvention. A protein encoded by the cDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can be used to detect a protein in a sample or purify a natural or recombinant protein from a sample. The nucleotides may be useful for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, cancer, coronary reperfusion injury, restenosis, or stroke. The cDNAs can also be used for large-scale genetic or gene expression analysis of several new nucleic acid molecules. Antibodies to the proteins encoded by the cDNAs are useful for diagnosing pre-pathologic disorders, and chronic or acute diseases associated with abnormalities in the expression, corpresents a cDNA of the protein. The present sequence corpresents a cDNA of the invention that is differentially expressed in activated vascular tissue.
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a combination comprising several cDNAs that are differentially expressed in activated vascular tissue. The invention also discloses a high throughput method for detecting differentially expressed cDNAs in a sample. The cDNAs of the invention may have
                                                                                                                                                                                                                                                                                                                                                                Agonist; antagonist; myeloid leukaemia; therapy; screening; diagnosis; granulocyte-macrophage colony stimulating factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence encoding beta-chain of a human granulocyte-macrophage colony stimulating factor (GM-CSF) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from USPTO at http.seqdata.uspto.gov/sequence.html?DocID=20020137081.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated vascular tissue -
                                      06-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3439 BP; 675 A; 1122 C; 999 G; 643 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The nucleic acid encoding the human GM-CSF beta-chain is isolated from a cDNA library prepd. from poly(A)+ RNA from TF-1 cells. The high affinity human GM-CSF receptor (Kd < 1 nM) can be used for screening candidate GM-CSF agonists and antagonists e.g. for
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P-PSDB; AAR20982.
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Query Match
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Matches 19
                                                 The invention relates to novel human receptor proteins and nucleic molecules encoding such proteins. The invention is useful for prepa a composition for treating a disease or condition mediated by a hum receptor protein e.g. leukaemia or cancer. The invention is also us in gene therapy. The present sequence is human receptor gene.
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Score 19; DB
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RESULT 10
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KW Viral
KW Fungal
KW Fungal
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                    CC (GCA), by detecting the level of expression of gene(s) (GS) identified by CC (DNA chip analysis as given in the specification, and comparing CC the expression level are expression of gene(s) (GS) identified by CC (GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a Subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from GS, where CC the level of expression of the gene is indicative of inflammation; (CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response of a subject to a pathogen or sterile inflammatory disease, by detecting the CC inflammation with an agent that modulates the expression of gene(s) from GS, where CC inflammation with an agent that modulates the expression of gene(s) constanting GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue, M4 is useful for cetecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile conflammatory disease (e.g. psoriasis, rheumatoid arthritis, conflammatory bowel disease, Crohn's disease, ulcerative colitis, conflammator, inputy, adult respiratory distress syndrome, and M5 is conflammation, conflammation, viral infection, and M5 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                inflammatory bower inflammatory 
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                           This is an antisense oligonucleotide directed against the common beta subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5) receptor and the granulocyte macrophage colony stimulating factor (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5 and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines involved in eosinophil proliferation and survival, they are increased in asthma and atopic diseases, and are also involved in the indefinite proliferation of certain neoplastic diseases. The invention relates to antisense oligonucleotides directed against a nucleic acid sequence encoding either a chemokine receptor (CCR3), a common subunit of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common subunit of IL-3, IL-5 and GM-CSF receptors. The antisense oligonucleotides can be used in the treatment or prevention of asthma, allergy, hypereosinophilia, general inflammation or cancer.
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The present invention relates to a method for increasing the in vivo cc efficacy of oligonucleotides and inhibiting inflammation. The oligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide cc substitutions are useful for increasing in vivo efficacy of a nucleic cardid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or creventing pulmonary/respiratory diseases, neurological diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, choners. The respiratory system diseases, urinary system diseases, cancers. The respiratory system diseases is a sickness associated with can inflammation of the lungs, the airways and/or the nose. The respiratory system disease is a sickness associated with can inflammation of the lungs, the airways and/or the nose. The respiratory distress syndrome, cystic fibrosis, chronic obstructive lung disease, chronic bronchitis, eosinophilic bronchitis, adult respiratory distress syndrome, cystic fibrosis, chronic obstructive DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. Chap or its analogues are more effective than other substitutes of adenosine. ABX12681-ABX12698 represent antisense oligonucleotides for treating or preventing atopic diseases and neoplastic cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involves incorporating nucleotide substitute
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Query Match

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other; DB 25;

Score 18;

Length

19;

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RESULT 14
ABX12690
       The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cutaneous diseases, rheumatological diseases, urinary system diseases, cardiovascular diseases, rheumatological diseases, urinary system diseases, cardiovascular diseases, general inflammation and cancers. The respiratory system disease is a sickness associated with an inflammation of the lungs, the airways and/or the nose. The respiratory distress syndrome, cystic fibrosis, chronic obstructive lung disease, chronic bronchitis, eosinophilic bronchitis, asthma, condified oligonucleotides are more stable in the body, more and least toxic than attached artisants of the body, more
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one
                                                                                                                                                                                                                                                                                                                                                                                       Claim 28; Page 11; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide substitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Renzi P,
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                         This is an antisense oligonucleotide directed against the common beta subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5) receptor and the granulocyte macrophage colony stimulating factor (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5 and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines involved in eosinophil proliferation and survival, they are increased in asthma and atopic diseases, and are also involved in the indefinite proliferation of certain neoplastic diseases. The invention relates to antisense oligonucleotides directed against a nucleic acid sequence encoding either a chemokine receptor (CCR3), a common subunit of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common subunit of IL-3, IL-5 and GM-CSF receptors. The antisense oligonucleotides can be used in the treatment or prevention of asthma, allergy, hypereosinophilia, general inflammation or cancer.
                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotides directed to CCR3, interleukin or granulocyte macrophage colony stimulating factor receptors, used for treating or preventing asthma, allergies, hypereosinophilia, inflammation or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide; asthma; allergy; cancer; receptor expression inhibitor; cytokine; inflammation; hypereosinophilia; eosinophil proliferation; granulocyte macrophage colony stimulating factor; GM-CSF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for treating or preventing atopic proliferation.
                                                                                                                                                                                                                                                                      Claim 5; Page 25; 72pp; English.
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Query Match Best Local Similarity

89.5%; 100.0%;

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                                                                      efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of 2.6. diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cardiovascular diseases, rheumatological diseases, digestive diseases, curinary system diseases, curinary system diseases, cancers. The respiratory system diseases, general inflammation and cancers. The respiratory system disease is a sickness associated with an inflammation of the lungs, the airways and/or the nose. The respiratory distress syndrome, cystic fibrosis, chronic obstructive lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
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allergy, allergic rhinitis, sinusitis and hypereosinophilia. The DAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. DAP or its analogues are more effective than other substitutes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy; DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; disease; disease; ophthalmological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis;
                                                     Examples;
                                                                                                       Increasing in vivo efficacy of a nucleic acid molecule that administered to a mammal for inhibiting inflammation in mamm involves incorporating into the nucleic acid molecule at lear nucleotide substitute -
                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-2001; 2001US-303071P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    atopic disease; neoplastic cell proliferation; antisense;
interleukin-3 receptor; interleukin-5 receptor; GM-CSF; su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypereosinophilia; cardiant; ophthalmological; cytostatic; antiasthmatic; antiallergic; antiinflammatory; immunosuppr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IL-3/IL-5/GM-CSF receptor DNA, antisense oligonucleotide 107A-DAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-2003
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                                                                                                                                                                                                                                                                                             Renzi P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-2002; 2002WO-CA01046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                 TOPIGEN PHARM
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                                                     18; 63pp; English
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/mod_base= OTHER
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= "OTHER= D
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Pred. No.
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                                                                                                                                                                 in mammals,
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The present invention relates to a method

for increasing the

in vivo

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RESULT 18
ABX12702
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ABX12
AC
ABX12
XX
DT 10-MA
XX
DE Human
KW Human
KW DAP-m
KW DAP-m
KW Cysti
KW Cysti
KW Giges
KW Winter
KW Atopi
KW A
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CC cardiovascular diseases, rheumatological diseases, digestive diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC cutaneous diseases, ophthalmological diseases, urinary system diseases,
CC pathogen infections, genetic diseases, general inflammation and
CC cancers. The respiratory system disease is a sickness associated with
CC an inflammation of the lungs, the airways and/or the nose. The
CC respiratory system disease is selected from pulmonary fibrosis, adult
CC respiratory distress syndrome, cystic fibrosis, chronic obstructive
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC lung disease, chronic bronchitis, eosinophilic bronchitis, asthma,
CC allergy, allergic rhinitis, sinusitis and hypereosinophilia. The
CC allergy, and less toxic than standard antisense oligonucleotides.
CC DAP or its analogues are more effective than other substitutes of
CC adenosine. The present sequence represents an antisense oligonucleotide
CC used in the examples of the present invention.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; inflammation; 2'6'-diaminopurine; DAP; antisense therapy; DAP-modified oligonucleotide; pulmonary disease; respiratory disease; neurological disease; cardiovascular disease; rheumatological disease; digestive disease; cutaneous disease; ophthalmological disease; urinary system disease; pathogen infection; genetic disease; cancer; airway; nose; pulmonary fibrosis; adult respiratory distress syndrome; cystic fibrosis; chronic obstructive lung disease; chronic bronchitis; eosinophilic bronchitis; asthma; allergy; allergic rhinitis; sinusitis; hypereosinophilia; cardiant; ophthalmological; cytostatic; antiasthmatic; antiallergic; antiinflammatory; immunosuppressive; atopic disease; neoplastic cell proliferation; antisease; IL-3; IL-5; into the content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         efficacy of oligonucleotides and inhibiting inflammation. The oligonucleotides comprise at least one nucleotide substitute of 2'6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide substitutions are useful for increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal. The DAP-modified oligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens Synthetic.
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                                         08-JUL-2002; 2002WO-CA01046
                                                                                                                              16-JAN-2003.
                                                                                                                                                                                                                WO2003004511-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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15
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Pred. No. 91;
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RESULT 19
AAK63218/c
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AC AAK632
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Human;
KW Cytost
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OS Homo 8
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OS Homo 8
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PN WO2001
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PF 17-JAN
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PF 17-JAN
PR 04-FEE
PR 24-FEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for increasing the in vivo efficacy of oligonucleotides and inhibiting inflammation. The coligonucleotides comprise at least one nucleotide substitute of CC 2'6'-diaminopurine (DAP) and/or its analogue. The DAP nucleotide cC substitutions are useful for increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal. The DAP-modified coligonucleotides are useful in antisense therapy for treating and/or preventing pulmonary/respiratory diseases, neurological diseases, cutaneous diseases, ophthalmological diseases, digestive diseases, cutaneous diseases, ophthalmological diseases, urinary system diseases, pathogen infections, genetic diseases, general inflammation and cancers. The respiratory system disease is a sickness associated with an inflammation of the lungs, the airways and/or the nose. The respiratory system disease is a sickness associated with crapitatory distress syndrome, cystic fibrosis, chronic obstructive lung disease, chronic bronchitis, eosinophilic bronchitis, adult respiratory distress syndrome, cystic fibrosis, chronic obstructive allergy, allergic rhinitis, sinusitis and hypereosinophilia. The CDAP-modified oligonucleotides are more stable in the body, more effective, and less toxic than standard antisense oligonucleotides. CDAP or its analogues are more effective than other substitutes of cused in the examples of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing in vivo efficacy of a nucleic acid molecule that is administered to a mammal for inhibiting inflammation in mammals, involves incorporating into the nucleic acid molecule at least one nucleotide substitute -
                                                                         17-JAN-2001;
                                                                                                                                                                                                                                                                                                                  06-NOV-2001
                                                                                                               09-AUG-2001
                                                                                                                                                                                                                      cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19
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                                                                                                                                                WO200157182-A2
                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         AAK63218;
                                                                                                                                                                                                                                                                                                                                                                                            AAK63218 standard; cDNA; 256 BP
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTCTGCNGCGGGNTGGT 19
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 ; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 0 A; 3 C; 10 G; 4 T; 2 other;
                                                                           2001WO-US01354.
                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allakhverdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
00-NOV-2000;
08-NOV-2000;
17-NOV-2000;
17-NO
                        Nucleic acids encoding useful for preventing, metastasis -
                                                                                WPI; 2001-483426/52.
P-PSDB; AAM90437.
                                                                                                                           Rosen
                                                                                                                                                        (HUMA-)
                                                                                                                        CA,
                                                                                                                                                        HUMAN GENOME
                                                                                                                           Barash
                                                                                                                                                                                  2000US-0237040.
2000US-0239937.
2000US-0241960.
2000US-0241787.
2000US-02411787.
2000US-02411809.
2000US-0241827.
2000US-02446174.
2000US-0246477.
2000US-0246477.
2000US-0246477.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246526.
2000US-0246611.
2000US-0246611.
2000US-0249211.
2000US-0249213.
2000US-0249216.
2000US-0249216.
2000US-0249218.
2000US-0251988.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-0251999.
2000US-0251999.
2000US-0251999.
                                                                                                                            SC,
                                                                                                                                                         SCI INC
                                      human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                           Ruben SM;
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16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
21-MAR-2000;
2000;
21-MAR-2000;
21-MAR-2000;
21-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-AUG-2000;
11-SEP-2000;
12-SEP-2000;
13-SEP-2000;
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29-SEP-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;

2000US-0225758.
2000US-0226279.
2000US-0226681.
2000US-0226681.
2000US-0227009.
2000US-0229343.
2000US-0229344.
2000US-0229344.
2000US-0229344.
2000US-0229343.
2000US-0230437.
2000US-0231242.
2000US-0231244.
2000US-0232399.
2000US-0234991.
2000US-0234998.
2000US-0234998.
2000US-0234998.
2000US-0234998.
2000US-0236367.
2000US-0236367.
2000US-0236369.
2000US-023637039.
2000US-023637039.

Claim 1; SEQ ID NO 8278; 3071pp + Sequence Listing; English

2000US-0220964 2000US-0224518 2000US-0224519 2000US-0225213 2000US-0225214 2000US-0225266 2000US-0225267 2000US-0225268 2000US-0225268 2000US-0225270 2000US-0225277 2000US-0225759 2000US-0225759 2000US-0225759

2000US-0205515. 2000US-0209467. 2000US-0214886. 2000US-0215135. 2000US-0216647. 2000US-0216880. 2000US-0217487. 2000US-0217496. 2000US-0217496.

2000US-0186350. 2000US-0189874. 2000US-0190076. 2000US-0198123.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For certifying mutations or deletions in a patient's genome certain the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement the patients own production of (I). Additionally, (I) complement in a host cell and culturing the cell to express the contein. (I) proteins and polynucleotides may be used to prevent, complement in treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 capresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 17
                                                                                                                                             08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
                                                                                                   14-JUL-1999;
27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum; stress; resistance; tolerance; SRT; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme;
                                                                                                                                                                                                                                                                                                            04-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C. glutamicum
               Pompejus M,
Kim H;
                                                                                                                                                                                                                     01-JUL-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                        08-JUL-1999;
                                                                                                                                                                                                                                                  25-JUN-1999;
                                                                                                                                                                                                                                                                                 23-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                  evolutionary study; environmental hazard; fermentation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF71002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF71002 standard; DNA; 436
                                                         (BADI )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
17; Conserv
                                                         BASF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 BP; 67 A; 71 C; 71 G; 46 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGTCTGCAGCAGGATGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                         გ
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                           Kroeger
                                                                                                                                                                                                                                                                                 2000WO-IB00922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRT protein nucleotide sequence SEQ ID NO:37
                                                                                                                              99DE-1031457.
99DE-1031541.
99DE-1032209.
99DE-1032230.
99DE-10322314.
                                                                                                                  99DE-1040764.
                                                                                                                                                                                                        99DE-1031413.
                                                                                                                                                                                                                      99US-0142692
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                                                                                                                                                                                                                                                   99US-0141031.
                                                                                                                                                                                                                                                                                                                                                                    glutamicum.
                           'n
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                           Schroeder H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 16.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+02;
                           Zelder O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                            Haberhauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                           ត្
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                           Lee
                           Ή
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RESULT 21
AAK84431/c
ID AAK844
XX
AC AAK844
XX
DT 07-NOV
XX
DE Human;
KW Human;
KW Cytost
XX
PM WO2001
XX
PM WO2001
XX
PF 17-JAN
PR 04-FEB
PR 02-MAR
PR 16-MAR
PR 11-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARF70984 to AAF71133 encode the Corynebacterium glutamicum stress, CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020. CC The C. glutamicum SRT genes (I) can be used in vectors (II) for CC expression in host cells and production of fine chemicals, such as, an CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred), CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid, a diol, a carbohydrate, an aromatic CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine CC chemical production can be modulated. The presence of (I) or the SRT proteins (III) encoded by them are used for diagnosing the presence or activity of Corynebacterium diphtheriae. (I), (II), (III) and host cells containing them can be used to map the genomes of organisms related to C. glutamicum, to identify and localise C. glutamicum sequences of cregions required for function, in modulating the SRT protein cregions required for function, in modulating the SRT protein activity, can an environment that is normally contained by it increase the survival of C. glutamicum to ourvive in an environment that is normally condended by it increase the survival of C. glutamicum to chemical and convironmental hazards and provide a means for continued growth and convironmental hazards and provide a means for continued growth and convict conditions, the yield, production and/or efficiency or production of fine chemicals from a culture may be increased.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated Corynebacterium glutamicum nucleic acid encoding a stress, tolerance or resistance protein, for production or modulation of production of fine chemicals, such as, e.g. amino acids, lipids,
                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2001
                                                                                                                              17-JAN-2001; 2001WO-US01354
                                                                                                                                                                   09-AUG-2001
                                                                                                                                                                                                                                                                              Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 172; 526pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbohydrates, or enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB78889.
                                                                                                                                                                                                      WO200157182-A2
                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                               AAK84431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK84431 standard; DNA; 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-061972/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                    immune/haematopoietic antigen genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTCTGCAGCGGGATGGT
; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
; 2000US-0186350.
; 2000US-0189874.
; 2000US-0190076.
                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%;
llarity 94.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 81 A; 102 C;
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                            therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; D
Pred. No. 2.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 G; 115 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                     SEQ ID NO:39243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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2000US-0198123. 2000US-0205515. 2000US-0209467.

2000US-0209467.
2000US-0215135.
2000US-0216647.
2000US-0217487.
2000US-0217487.
2000US-0218290.
2000US-02218290.
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2000US-0224518.
2000US-0225214.
2000US-0225214.
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2000US-0225267.
2000US-0225270.
2000US-0225270.
2000US-0225277.

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20-OCT-2000;

20-OCT-2000;

20-OCT-2000;

20-OCT-2000;

20-OCT-2000;

01-NOV-2000;

08-NOV-2000;

17-NOV-2000;

17
                                                                                           Nucleic acids encoding useful for preventing, metastasis -
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I)
                                                                                                                                                          WPI;
                                                                Disclosure;
                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                      (HUMA-)
                                                                                                                                                          2001-483426/52
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                                                                                                                                                                                                                       HUMAN
                                                                                                                                                                                          Barash
                                                                                                                                                                                                                                                    2000US-0240960.
2000US-0241785.
2000US-0241787.
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2000US-0241809.
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2000US-0249218.
2000US-02511868.
2000US-02511869.
2000US-0251989.
2000US-0251989.
                                                                SEQ
                                                                                                                                                                                                                        GENOME
                                                              ID NO 39243; 3071pp +
                                                                                                                                                                                          sc,
                                                                                                                                                                                                                         SCI
                                                                                                             human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                           Ruben
                                                                                                                                                                                           MS,
                                                             Sequence Listing; English.
                                                                                                              antigen
cancers
                                                                                                                polypeptides, and
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18-APR-2000;
19-MAY-2000;
207-JUN-2000;
11-JUL-2000;
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11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-AUG-2000;
11-SEP-2000;
12-SEP-2000;
12-SEP-2000;
13-SEP-2000;
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13-SEP-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;

2000US-0225758.
2000US-0226681.
2000US-0226681.
2000US-0226681.
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2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229343.
2000US-0229509.
2000US-0239343.
2000US-0231243.
2000US-0231243.
2000US-0231244.
2000US-0233299.
2000US-0233299.
2000US-0233299.
2000US-0233299.
2000US-0234299.
2000US-0234299.
2000US-0234299.
2000US-0235363.
2000US-0235363.
2000US-0235363.
2000US-02356327.
2000US-0236369.
2000US-0237039.
2000US-0237039.
2000US-0237039.
2000US-0237039.
2000US-0237039.
2000US-0239935.

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RESULT 22
AAK84430/c
AAK84430 standard; DNA; 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 17
04-FEB-2000;
24-FEB-2000;
16-MAR-2000;
16-MAR-2000;
18-APR-2000;
19-MAY-2000;
28-JUN-2000;
28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAKS4942 to AAKS4950 and AAK82169 are protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 535 BP; 148 A; 159 C; 143 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                    31-JAN-2000;
                                                                                                                                                                                                                                                                                                                                            17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                             WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGTCTGCAGCAGGATGG 189
2000US-019874

2000US-0199076

2000US-0198123

2000US-0205515

2000US-0214886

2000US-0216647

2000US-0216880

2000US-0217487

2000US-0217487

2000US-0217496

2000US-0217496

2000US-0217496

2000US-02217496

2000US-02217496

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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2000US-0180628.
2000US-0184664.
2000US-0186350.
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Pred. No. 2.
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    01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
14-SEP-2000;
14-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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29-SEP-2000;
29-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
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08-NOV-2000;
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12-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
14-SEP-2000;
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01-SEP-2000;
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30-AUG-2000;
                                                                                                                                                                                       2000US-0225447.
2000US-0225758.
2000US-0225759.
2000US-02268681.
2000US-02268681.
2000US-02268681.
2000US-02268682.
2000US-0227009.
2000US-0229287.
2000US-0229287.
2000US-0229344.
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2000US-0231244.
2000US-0231249.
2000US-0231249.
2000US-0233299.
2000US-0234297.
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2000US-0234298.
2000US-0234298.
2000US-0234299.
  2000US-0241808.

2000US-0241809.

2000US-0244617.

2000US-0246474.

2000US-0246475.

2000US-0246477.

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2000US-0246523.

2000US-0246524.

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2000US-0246527.
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2000US-0246532

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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17-NOV-2000;
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                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 39242; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483426/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-2000;
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2000US-0251989.
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2000US-0249215.
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2000US-0249210.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
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Query Match 86.3%; Best Local Similarity 94.4%; Matches 17; Conservative

Score 16.4; DB 22; Pred. No. 2.1e+02; 0; Mismatches 1;

Length 536;

Indels

0;

Gaps

0

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Matches Query Match Best Local (

17; Conservative

GGTCTGCAGCGGGATGGT

19 <u>,</u>

h 86.3%; Similarity 94.4%;

Score 16.4; DB 23; Length Pred. No. 2.2e+02;

825;

<u>ب</u>

Indels

0

Gaps

0

Sequence 536

B₽;

146

A; 161 C; 143 G;

86 T; 0 other;

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                          polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The conversal activity of (II) is useful in gene therapy techniques cc to restore normal activity of (II) or to treat disease states involving cc (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cc disgress involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cc and to produce other types of data and products dependent on DNA and canino acid sequences. AAS64197-AAS94564 represent novel human cc diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at figure in the pub/published pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
Sequence
                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 3510; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #3510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-639362/73.
DB; ABG03519.
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825
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BP; 156 A; 278
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 C; 267 G; 124 T; 0 other;
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899

GGTCTGCAGCGGGACGGT 682

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                                                                                                                                                     The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC dispreders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cc and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published_pct_sequences.
                                                       Query Match
Best Local Similarity
Matches 17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 19270; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #19270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-FEB-2002
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899
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                                                                                                                                825 BP;
 GGTCTGCAGCGGGACGGT 685
                             GGTCTGCAGCGGGATGGT 19
                                                               Conservative
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                                                                                                                                157
                                                                            86.3%;
94.4%;
                                                                                                                             A; 285 C; 258 G; 125
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                                                           Score 16.4; D
Pred. No. 2.2e
0; Mismatches
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                                                                            2.2e+02;
                                                                                           DB 23; Length 825;
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                                                               Indels
                                                               0
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Matches Query Match Best Local (

al Similarity 94.4 17; Conservative

86.3%;

Score 16.4; DB 21; Pred. No. 2.2e+02;

Length 1095;

0;

Mismatches

Indels

0

Gaps

0

2 GGTCTGCAGCGGGATGGT 19

Sequence 1095 BP; 210 A; 336 C; 273 G; 276 T; 0

other;

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RESULT 25
AAA72267;
AAA72267;
XX
AC AAA72267;
XX
Drosophila odorant receptor DORL
XX
Drosophila odorant receptor; GPCR
XX
Drosophila melanogaster.
XX
PN
W0200043410-A2.
XX
PN
W27-JUL-2000.
XX
25-JAN-2000; 2000WO-US01823.
XX
ZX
ZY
PN
W25-JAN-1999; 99US-0117132.
XX
ZX
ZY
PN
W27-JUL-2000.
XX
ZS-JAN-2000; 2000WO-US01823.
XX
ZS-JAN-2000; 2000WO-US01823.
XX
XX
PP
Carlson JR, Kim J, Clyne PJ,
XX
WPI; 2000-543246/49.
PR
Carlson JR, Kim J, Clyne PJ,
XX
Claim 3; Page 214-216; 303pp; Er
XX
New nucleic acid encoding a Dros
PT identifying modulating agents -
XX
Claim 3; Page 214-216; 303pp; Er
XX
Claim 3; Page 2
                                                                                                               Sequences AAA72236-A72284 represent cDNAs encoding Drosophila
CC melanogaster odorant receptors (AAB20901-B20949). These proteins function
CC as olfactory receptors, and are thought to be members of the G
CC protein-coupled receptors, and are thought to be members of the G
CC protein-coupled receptors, and are thought to be members of the G
CC protein-coupled receptors may be used to generate expression
CC constructs, host cells containing such constructs, and transgenic
CC insects. Cells which express the odorant receptor genes may be used in
CC methods to identify agents which modulate expression of these genes, and
CC receptor nucleic acids may also be used to identify corresponding genes
CC in other insects, such as those which damage crops or transmit disease.
CC The odorant receptor proteins may be used to identify agents which
CC modulate their activity, to identify binding partners, as antigens to
CC modulate their activity, to identify insect behaviour. The proteins
CC may be also be used in methods of behaviour modification. Such methods
CC such as pheromones. Modification of insect behaviour in response to odorants
CC applications, such as in pest control (e.g., by disrupting the feeding
CC and/or nucleotides may also be used to identify suppetite suppressants, to
CC and/or nucleotides may also be used to identify suppetite suppressants, to
CC and/or such as in pest control (e.g., by disrupting the feeding
CC and/or nucleotides may also be used to identify suppetite suppressants, to
CC trap odours of a specific type, as biosensors for the detection of
CC chiefly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Odorant receptor; Drosophila; olfactory receptor; g protein-coupled receptor; GPCR superfamily; transgenic insect; insect behaviour modification; pest control; pollinator attraction; biosensor; odour detection; odour identification; apiculture; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding a Drosophila olfactory receptor, useful identifying modulating agents - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 214-216; 303pp; English.
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RESULT 26
AAA94826/c
ID AAA94826;
XX
AC AAA94826;
XX
AC AAA94826;
XX
C 23-FEB-2001 (first entry)
XX
Drosophila melanogaster odorant
XX
Odorant receptor; fruit fly; DC
XX
C Drosophila melanogaster.
XX
C 31-AUG-2000.
XX
C 31-AUG-2000.
XX
C 31-AUG-2000.
XX
C 25-FEB-1999; 99US-0257706.
XX
C 25-FEB-2000; 2000WO-US04995.
XX
C 25-FEB-2000; 2000WO-US04995.
XX
C 25-FEB-2000; 2000WO-US04995.
XX
C 25-FEB-1999; 99US-0257706.
XX
C 25-FEB-2000; 2000WO-US04995.
XX
C 25-FEB-2000; 2000WO-US
RESULT 27
ABL06359/c
ID ABL06359 standard; cl
XX
AC ABL06359;
XX
XX
DT 26-MAR-2002 (first 4)
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Best Local
                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the coding sequence for the previously identified Drosophila melanogaster odorant receptor DOR119. The odorant genes and proteins, such as those provided by the invention, are useful as they aid in the study of the olfactory organ in mammals, as well as aiding the understanding of the link between odour recognition and behaviour in insects. They also enable the identification of compounds capable of activating and inhibiting the receptors, allow the control of pest populations via the use of alarm odour ligands and via the use of ligands which interfere with the interaction between odorant ligands and receptors associated with fertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Movel nucleic acid encoding an insect odorant receptor, modulator compounds that are useful in controlling pest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster odorant receptor DOR119 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Odorant receptor; fruit fly; DOR119; odour recognition; pest control;
                                                                                                                                                                                                                                                                                                                                                                       Sequence 1194 BP; 237 A; 360 C; 307 G; 290 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 58; 176pp; English.
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                                                                                                                                                                                                                                                                                   l Similarity
17; Conserva
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                                                                                                                                                                                                  GGTCTGCAGCAGGATGGT
                                                                                                                                                                                                                                          GGTCTGCAGCGGGATGGT 19
                                                                                                                                                                                                                                                                                     Conservative
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     (first entry)
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                                                                                        CDNA; 1197 BP
                                                                                                                                                                                                                                                                                                        86.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "DOR119"
                                                                                                                                                                                                  916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             832
                                                                                                                                                                                                                                                                                  Score 16.4; DI
Pred. No. 2.2e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                          2.2e+02;
                                                                                                                                                                                                                                                                                                                             DB 21;
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                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                 1194;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental pharmaceutical; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                           Sequence 1197 BP;
                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13559; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEKE)
                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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                                                                            17;
                                                                                                Similarity
                              GGTCTGCAGCGGGATGGT
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                                                                            Conservative
                                                                                                                                                             239 A; 360 C; 307 G;
                                                                                             86.3%;
94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
916
                                                                            Score 16.4; DB 23
Pred. No. 2.2e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers
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H
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ABQ90060/
ID ABQ9
XX ABQ9
XX O1-O
XX O1-O
XX Micr
XX Micr
XX Meth
XX WO20
XX WO20
XX X 18-J
XX X
                                                                                                                                                                                             RESULT 28
                                                                     Methylococcus capsulatus
                                                                                        Micro array; gene; ds; differential expression; gene expression.
                                                                                                            M. capsulatus gene #45 for DNA array.
                                                                                                                                   01-OCT-2002
                                                                                                                                                       ABQ90060,
                                                                                                                                                                         ABQ90060 standard; DNA; 1320
                              18-JUL-2002.
                                                                                                                                   (first
                                                                                                                                   entry)
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14-JAN-2002; 2002WO-NO00019

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RESULT 29.
ABQ90381
ID ABQ903
XX
AC ABQ903
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AC ABQ903
XX
DT 01-OCT
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Micro
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Micro
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Micro
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Mo2002
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PN WO2002
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                         12-JAN-2001;
12-JAN-2001;
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Lillehaug JR,
Novel DNA array useful for Methylococcus capsulatus oligonucleotides represer
                                                                                                                                                        Birkeland NK,
Lillehaug JR,
                                                                                                                                                                                                                                                                                                                                                               14-JAN-2002; 2002WO-NO00019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylococcus capsulatus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABQ90381;
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12-JAN-2001; 2001NO-0000239.
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17; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene;
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                                                                                                                                                                                                                                                                                             2001NO-0000239
                                                                                                                                                                                                                                                                                                                   2001NO-0000235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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Lossius I, Eisen JA,
                                                                                                                                                          Eidhammer I, Jonassen
Lossius I, Eisen JA,
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 psulatus genes, representative
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94.4%;
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 for determining differential expression of us genes, comprises polynucleotides or sentative for a selective number of Methylo
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Pred. No. 2
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Fraser
                                                                                                                                                          I, Jensen HB, Lien Traser CM, Durkin AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 T; 0 other;
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ser CM,
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Durkin
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     of Methylococcus
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scale and in
shown in
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Best Local S
Matches 17
            This invention describes novel isolated nucleic acid molecules (I) encoding a human secreted proteins (II) which have immunosuppressive, antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective, antibacterial, virucide, fungicide, ophthalmological and vulnerary activity and can be used for gene therapy. (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; vulnerary; gene therapy; treatment; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; ocular disorder; cerebrovascular disorder; nervous system disorder; infection; skin aging; wound healing; epithelial cell proliferation; transplantation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                             Nucleic acid molecules encoding human secreted preventing, treating or ameliorating a disorder Parkinson's diseases and cancers -
                                                                                                                                                                                                                           WPI; 2000-611704/58.
P-PSDB; AAB45044.
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                                                                                                                                  Claim la; Page 351-352; 418pp; English.
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07-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME
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17; Conserv
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                                                                                                                                                                                                                                                                      SM,
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94.4%;
                                                                                                                                                                                                                                                                                                   SCI INC
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Pred. No. 2.3e+02;
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in e.g. humans,
sheep. (I) and
                                                                                                                                                                                                                                                                      <u>ن</u>
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                                                                                                                                                                                disorder,
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                                                                                                                                                                           proteins, used in
r, e.g. Alzheimer's
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cc diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to (II) can also be used in alleviating cc symptoms associated with the disorders and in diagnostic immunoassays ce.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases cc e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms cf the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, crivases and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, corneal as a food additive or preservative to increase or decrease storage capabilities.
      RESULT 31
AAH65074
ID AAH65
XX
AC AAH65
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AC AAH65
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CO-SE
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Best Local (
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium; organic acid synthesis
The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. are useful for identifying the mutation point of a gene derived from mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived derived the corynery of a gene derived the presence of the corynery of the expression profile or expression pattern of a gene derived the profile of the corynery of the c
                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2000;
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                                                                                                                                                                                                                                                                  Claim
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17; Conser
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                                                                                                                                                                                                                                                                  SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 99JP-0377484.
; 2000JP-0159162.
; 2000JP-0280988.
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Senoh A, Ikeda M, Ozaki A;
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s; ds.
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Pred. No. 2.
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RESULT 32
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Matches 17
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; evolutionary study; environmental hazard; fermentation; ds.
                                                                                                                                                                                                                                                            Pompejus
Kim H;
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                          Claim
                                                                                              production of fine chemicals, su
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01-JUL-1999
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27-AUG-1999;
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                                                                                                               isolated Corynebacterium glutamicum nucleic acid encoding erance or resistance protein, for production or modulation
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                                                                                                                                                                                                                                                                                   Z,
                        Page 166-169; 526pp; English
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99DE-1032230.
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99DE-1040764.
99US-0151214.
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99DE-1031413.
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94.4%;
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Pred. No. 2.
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CC resistance, and tolerance (SRT) proteins given in AAB78871 to AAB79020.
CC The C. glutamicum SRT genes (I) can be used in vectors (II) for
CC expression in host cells and production of fine chemicals, such as, an
CC organic acid, a proteinogenic or nonproteinogenic amino acid (preferred),
CC a purine or pyrimidine base, a nucleoside, a nucleotide, a lipid, a
CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine
CC compound, a vitamin, a cofactor, a polyketide, or an enzyme. The fine
CC chemical production can be modulated. The presence of (I) or the SRT
CC proteins (III) encoded by them are used for diagnosing the presence
CC cells containing them can be used to map the genomes of organisms related
CC cells containing them can be used to map the genomes of organisms related
CC conjutamicum, to identify and localise C. glutamicum sequences of
CC interest, in evolutionary studies, in determination of SRT protein
CC glutamicum to survive in an environment that is normally
CC environmentally or chemically hazardous to it. (I) and protein activity,
CC environmentally or chemically hazardous to it. (I) and protein molecules
CC encoded by it increase the survival of C. glutamicum to chemical and
CC environmental hazards and provide a means for continued growth and
CC environmental hazards and provide a means for continued growth rate in poor or
CC continued growth rate or maintaining a normal growth rate in poor or
CC continued growth rate or maintaining a normal growth rate in poor or
CC continued growth rate or maintaining a normal growth rate in poor or
CC of fine chemicals from a culture may be increased.
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Matches 17
                             Claim
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11-JUL-2000; 2000US-0614150.
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pharmaceutical;
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                                                                                             interactions
                                                                                                                 New isolated nucleic acid genes from Drosophila and
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  This sequence encodes a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be use to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist
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                                                                                                                                                                                             Claim 4; Fig
                                                                                                                                                                                                                                                   Proteins containing scavenger receptor, cysteine rich useful for diagnosis and treatment of tumours
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09-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Mollenhauer J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-1998;
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        The invention relates to novel isolated nucleic acid molecules (I) CC encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, CC goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with CC inappropriate expression of secreted proteins. (I) and complementary gequences may also be used as DNA probes in diagnostic assays (e.g. CC polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The condition of antibodies immune/autoimmune diseases (e.g. HIV) and intibodies and multiple aclassion and activity of the secreted conditions of the secreted proteins.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancer multiple sclerosis; cancer; hyperproliferative disorder; infection; Gaucher's disease; neurological disease; cerebrovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids and polypeptides, useful for diagnosing, preventing or treating medical conditions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-JAN-2000; 2000US-0179065.
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Pred. No. 2.
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RESULT 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerebroprotective; thrombolytic; antimicrobial; ophthalmological; cytostatic; Alzheimer's disease; Parkinson's disease; human; cancemultiple sclerosis; cancer; hyperproliferative disorder; infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple sclerosis; cancer; hyperproliferative Gaucher's disease; neurological disease; cerebr
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rheumatoid arthritis; antiarteriosclerotic; cardiant; vascular;
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                                                                                                                                        Disclosure; SEQ ID No 696; 753pp; English.
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p medical com
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                                                                                                                                                                    nd polypeptides, useful for diagnosing, preventing conditions -
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bred. No. 2.5e+02;
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The invention relates to novel isolated nucleic acid molecules (I) encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may

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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
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                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
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/e J, Zhang Y,
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Pred. No. 2.5e+02
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RESULT 38
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Note: The sequence data for this patent did not form part of the printed expecification, but was obtained in electronic format directly from WIPO
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scavenger receptor cysteine rich domain; SRCR; diagnosis; nervous system; medullo-blastoma; glioma; breast; detectic autoantibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               18-JUL-1997;
09-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SC3 DNA.
                                                                                   Disclosure; Fig 5c; 54pp; German.
                                                                                                                                                                                                                                     WPI; 1998-399136/34.
                                                                                                                                                                                                                                                                                            Mollenhauer J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1998
                                                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT
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17; Conserv
                                                                                                                                                 containing scavenger receptor, or diagnosis and treatment of to
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                                                                                                                                               diagnosis
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97DE-1000519.
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                                                                                                                                               and treatment
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Pred. No. 2.
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?.6e+02;
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This nucleotide sequence contains a fragment of a gene of encoding a protein which contains a SRCR (scavenger

which is capable receptor,

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RESULT 39
AAH64966/c
ID AAH649
XX AAH649
XX AAH649
XX CAYNE
DE C glut
XX Coryne
KW Coryne
KW organi
XX COryne
XX EP1108
XX INAWAGA
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                                                  sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999;
07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of nucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2000;
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17; Conser
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2000JP-0159162.
2000JP-0280988.
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Senoh A, Ikeda
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94.4%;
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da M, Ozaki A;
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   English
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RESULT 40
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Best Local S
Matches 17
                                                                                                                    This is an antisense oligonucleotide directed against the common beta subunit of the interleukin-3 (IL-3) receptor, the interleukin-5 (IL-5) receptor and the granulocyte macrophage colony stimulating factor (GM-CSF) receptor. The antisense oligonucleotide inhibits IL-3, IL-5 and GM-CSF receptor expression. IL-3, IL-5 and GM-CSF are cytokines involved in eosinophil proliferation and survival, they are increased in asthma and atopic diseases, and are also involved in the indefinite proliferation of certain neoplastic diseases. The invention relates to antisense oligonucleotides directed against a nucleic acid sequence encoding either a chemokine receptor (CCR3), a common subunit of interleukin-4 (IL-4) and interleukin-13 (IL-13) receptors, or a common oligonucleotides can be used in the treatment or prevention of asthma, allergy, hypereosinophilia, general inflammation or cancer.
                                       Matches
                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           asthma; allergy; cancer; receptor expression inhibitor; cy inflammation; hypereosinophilia; eosinophil proliferation; granulocyte macrophage colony stimulating factor; GM-CSF;
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                                                                                                                                                                                                                                                                                                                                                                                    Antisense oligonucleotides directed to CCR3, interleukin or granulocyte macrophage colony stimulating factor receptors, used for treating or preventing asthma, allergies, hypereosinophilia, inflammation or cancer
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                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                          Claim 5; Page 25; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interleukin-3; IL-3; interleukin-5; IL-5; antisense oligonucleotide;
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17; Conserv
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                                                    Similarity
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          GGGTCTGCAGCGGGAT 16
                                    84.2%; Solitarity 100.0%; Conservative 0;
                                                                                               BP; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPERTISES & DEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-CA00572
                                                                                             A; 4 C; 9 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79703 A; 91547 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16.4; DB Pred. No. 3e+02
                                                    Score 16;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDICAUX PARENZ IN
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                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3e+02;
                                                    DB 21; I
2.7e+02;
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                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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